

STIC-Biotech/ChemLib

89049

From: Bunner, Bridget
Sent: Friday, March 14, 2003 8:01 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/686,020:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

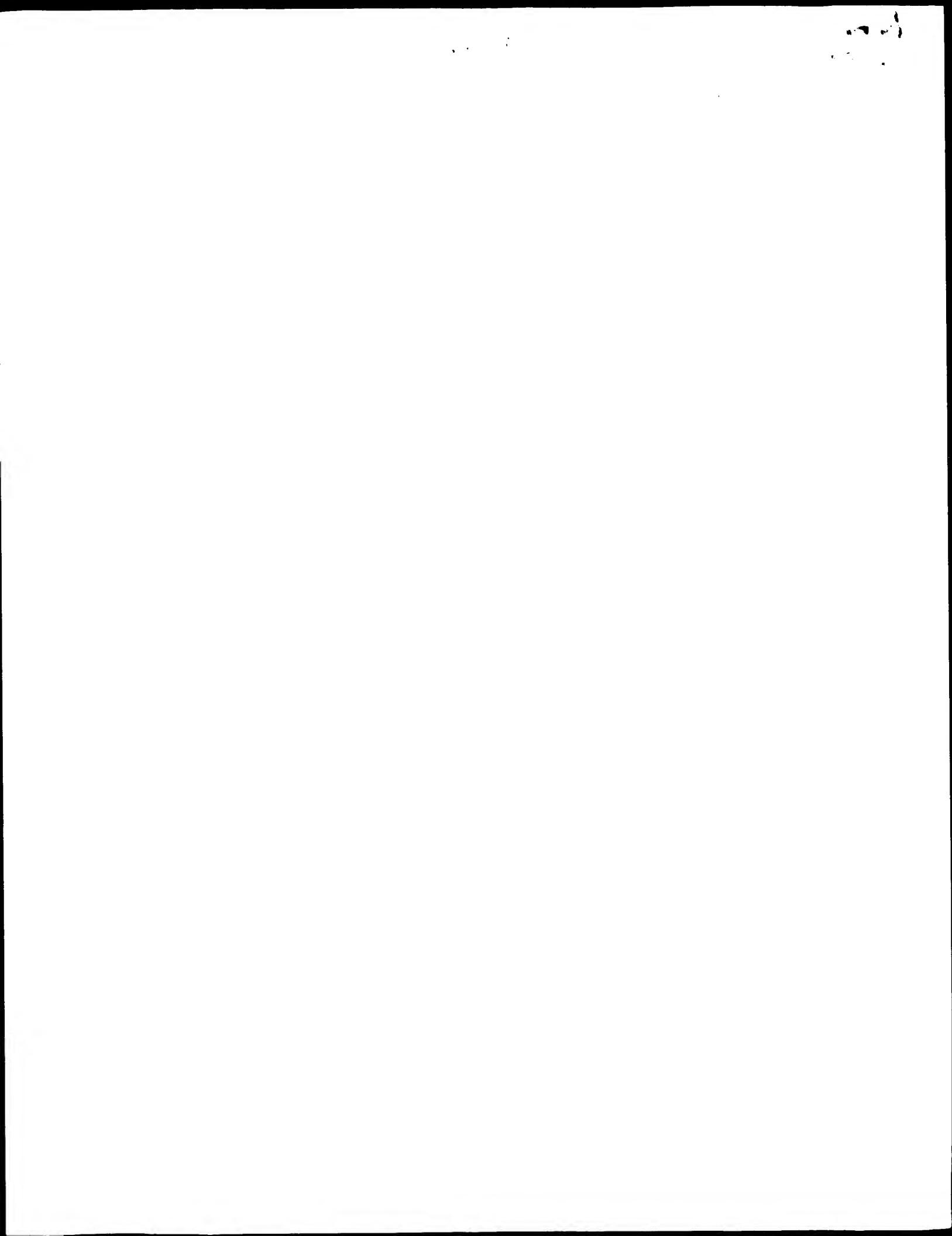
Art Unit 1647
CMI-10D12
(703) 305-7148
mailbox 10B19

Point of Contact:
Beverly Shears
Technician Info. Specialist
CM1 1605 Tel: 308-4994

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

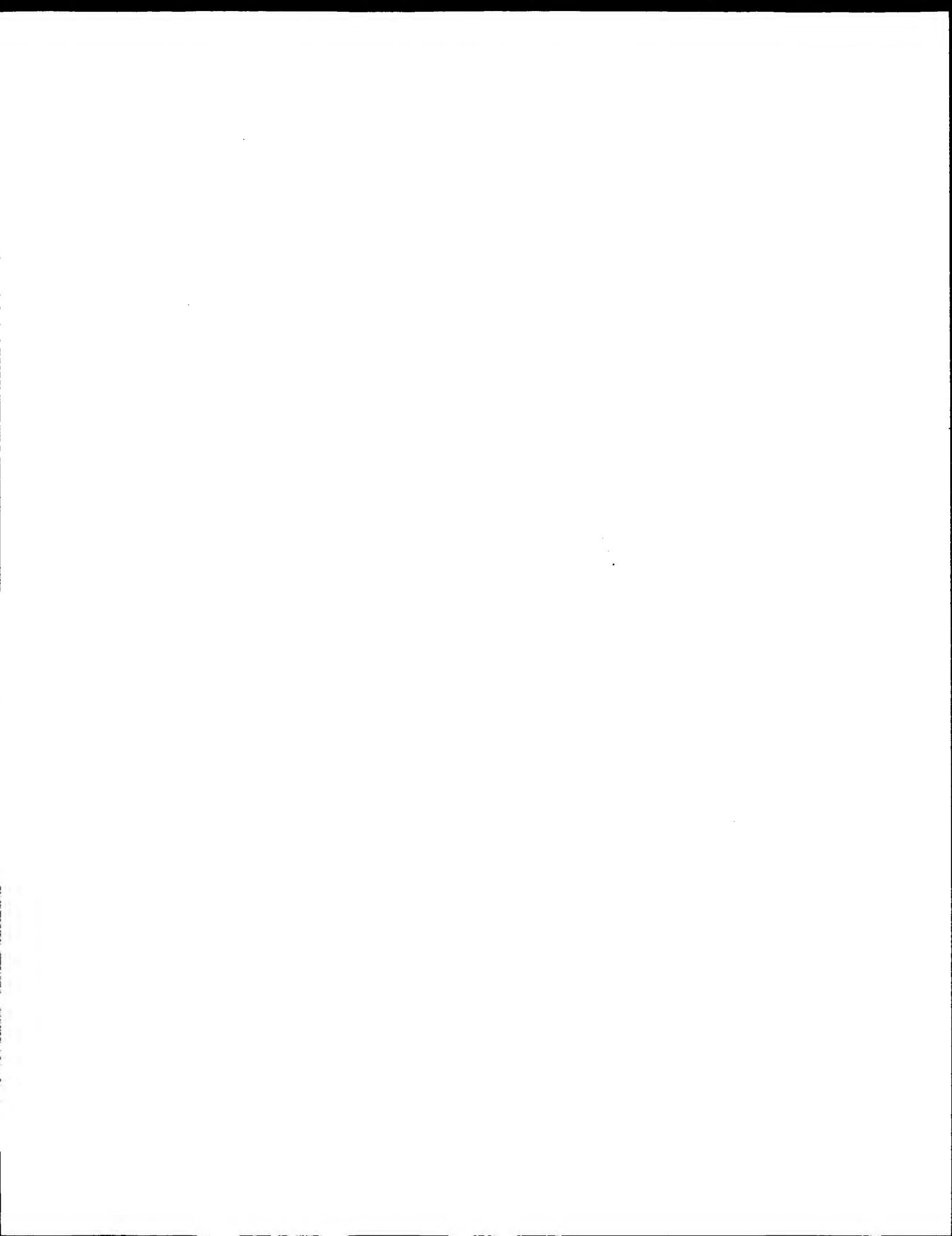
Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors key words, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 03-17-03
Searcher: Beverly e4994
Terminal time: 20
Elapsed time:
CPU-time:
Total time: 23
Number of Searches:
Number of Databases: 1

Search Site	Vendors
STIC	IG Suite
CM-1	STN
Pre-S	Dialog
Type of Search	
N.A. Sequence	APS
A.A. Sequence	Geninfo
Structure	SDC
Bibliographic	DARC/Questel
	Other CGN



OM protein - protein search, using sw model
 Perfect score: US-09-686-020a-2
 Sequence: 1 MALEQNQSTDYYEENEMNG VEEFPFDSEGPTEPSTFSI 350

Run on: March 14, 2003, 16:07:45 ; Search time 11 Seconds
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : SwissProt_40.*

Result No.	Score	Query	Match Length	DB	ID	Description	
1	1819	100.0	350	1	CKRB_HUMAN	Q9nb9 homosapiens	
2	1620	89.1	350	1	CKRB_BOVIN	P35509 bovis taurinus	
3	659	36.2	378	1	CRR7_HUMAN	P32248 homosapiens	
4	659	35.7	378	1	CRR7_MOUSE	P47776 mus musculus	
5	639	35.1	369	1	CRR9_MOUSE	Q9wq17 mus musculus	
6	637	35.0	357	1	CRR9_HUMAN	P51686 homosapiens	
7	7	33.3	367	1	CKR6_MOUSE	Q54689 mus musculus	
8	583	32.1	374	1	CKR6_HUMAN	P51684 homosapiens	
9	581	31.9	342	1	CCR6_CERAE	Q18833 cercopithecus aethiops	
10	571	31.4	343	1	CCR6_MACMU	Q9xt45 macacus mulatta	
11	569	31.3	342	1	CCR6_MACNE	O19024 macacus nemestrinus	
12	560	30.8	342	1	CCR6_HUMAN	O0574 homosapiens	
13	537.5	29.5	360	1	CCR4_HUMAN	P51779 homosapiens	
14	534.5	29.4	360	1	IL8B_HUMAN	P25025 homo sapiens	
15	529.5	29.1	353	1	IL8B_PANTHERA	Q28807 pan troglodytes	
16	527	29.0	384	1	CRD6_MACMU	O00590 homosapiens	
17	525	28.9	362	1	CKRA_HUMAN	P46092 homo sapiens	
18	524	28.8	354	1	C3X1_RAT	P35411 rattus norvegicus	
19	522.5	28.7	353	1	IL8B_GORGO	Q28422 gorilla gorilla	
20	522.5	28.7	355	1	C3X1_HUMAN	P49338 homo sapiens	
21	522.5	28.7	360	1	CKR4_MOUSE	P51680 mus musculus	
22	521.5	28.7	353	1	IL8B_MACMU	Q28519 macacus mulatta	
23	520.5	28.6	362	1	CKRA_MOUSE	O9J121 mus musculus	
24	512	28.1	356	1	IL8B_CANFA	O9J571 canis familiaris	
25	511	28.1	354	1	C3X1_MOUSE	Q9Q0D9 mus musculus	
26	511	28.1	358	1	IL8B_RABBIT	P35344 oryctolagus cuniculus	
27	504	27.7	360	1	CKR2_MACMU	O18793 macaca mulatta	
28	501.5	27.6	355	1	IL8A_RABBIT	P21109 oryctolagus cuniculus	
29	500.5	27.5	358	1	CKR3_CAVPO	Q9ZC13 cavipora porcata	
30	499	27.5	352	1	CKR4_HUMAN	P30391 homo sapiens	
31	499.5	27.5	353	1	P29330 bos taurus	P29330 bos taurus	
32	499.5	27.5	360	1	IL8B_BOVIN	Q28003 bos taurus	
33	498.5	27.4	352	1	CKR5_CERTO	P62743 cercopithecus aethiops	
34				353	CC	P56498 felis silvestris	
35				1	CCRA_FELCA	P55919 gorilla gorilla gorilla	
36				352	1	CKR5_CERAE	P5693 cercopithecus aethiops
37				1	CCR4_CERIO	Q28474 macaca fasciata	
38				352	1	CCR4_MACM	P79394 macaca mulatta
39				1	CCR4_MACMU	P54814 rattus norvegicus	
40				352	1	CCR4_RAT	P35407 rattus norvegicus
41				1	IL8B_RAT	P25641 papio hamadryas	
42				359	1	CKR5_PAPHA	P07880 pygathrix bengalensis
43				352	1	CKR5_PYGBI	P79436 macaca mulatta
44				352	1	CKR5_MACMU	
45				27.0			

ALIGNMENTS

Searched: 112892 seqs, 41476328 residues
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

ID	CKRB_HUMAN	STANDARD;	PRN;	350 AA.
CKRB_HUMAN				
SEQUENCE FROM N.A.				
RX	MEDLINE-20171478; Pubmed=10734104;			
RA	Schweickart V.L., Epp A., Raport C.J., Gray P.W.;			
RT	"CCR1 is a functional receptor for the monocyte chemoattractant protein family of chemokines."			
RT	J. Biol. Chem. 275:9550-9556(2000).			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-20200450; Pubmed=10766668;			
RA	Golding J., Daireighi D.J., Wang Y., Hanley M., Talbot D., Miao Z., Schall T.J.;			
RT	"Cutting edge: identification of a novel chemokine receptor that binds dendritic cell- and T cell-active chemokines including ELC, SLC, and TECK."			
RT	J. Immunol. 164:2851-2856(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-20171478; Pubmed=10767544;			
RA	Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.;			
RT	"Cloning of CCR1, an orphan seven transmembrane receptor related to chemokine receptors, expressed abundantly in heart."			
RT	Gene 246:229-238(2000).			
RL	-- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4, SCYA19/MIP3/ELC, SCYA21/SLC AND SCYA25/TECK.			
CC	-- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART. LOWER EXPRESSION IN LUNG, PANCREAS, SPLEEN, SMALL INTESTINE AND FETAL TISSUES.			
CC	-- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
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CC	EMBL; AF233281; AAF4751.1; -			
DR	EMBL; AF110640; AAF59827.1; -			

DR Genew; HGNC:1611; CCRL1
DR InterPro; IPR00216; GPCR_Rhodpsn.
DR Pfam; PF0001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS05062; G-PROTEIN RECEPTOR_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 43 63 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 64 87 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 88 108 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 109 113 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 114 134 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 135 154 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 155 175 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 222 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 223 240 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 241 261 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 262 289 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 290 310 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 311 350 EXTRACELLULAR (POTENTIAL).
FT CARTHRYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARTHRYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 112 184 BY SIMILARITY.
SQ SEQUENCE 350 AA; 39913 MW; 8E26049D2D575C8 CRC64;
Query Match 100.0%; Score 1819; DB 1; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.2e-103; O; Mismatches 0; Indels 0; Gaps 0;
Matches 350; Conservative 0; MisMatches 0; DR PROSITE; PS05062; G-PROTEIN RECEPTOR_F1_2; 1.
1 MALEQNSDSTYYEENEMGTYDSQEYELICKEDVREFAKVELPVLTIVFVLAGNS 60
1 MALEQNSDSTYYEENEMGTYDSQEYELICKEDVREFAKVELPVLTIVFVLAGNS 60
61 MVAIAYYKKRKRTDYTLNLAVADLFLTLPEWANAVHGWLKGKMRCKITSALYT 120
61 MVAIAYYKKRKRTDYTLNLAVADLFLTLPEWANAVHGWLKGKMRCKITSALYT 120
61 MVAIAYYKKRKRTDYTLNLAVADLFLTLPEWANAVHGWLKGKMRCKITSALYT 120
61 MVAIAYYKKRKRTDYTLNLAVADLFLTLPEWANAVHGWLKGKMRCKITSALYT 120
121 LNFGVSGMQLFACTISIDRVYAVTKVPSQSGVGKPCWICFCVWMAAIIISIPOLVFVYND 180
121 LNFGVSGMQLFACTISIDRVYAVTKVPSQSGVGKPCWICFCVWMAAIIISIPOLVFVYND 180
121 LNFGVSGMQLFACTISIDRVYAVTKVPSQSGVGKPCWICFCVWMAAIIISIPOLVFVYND 180
181 NARCIPPFRLGTSKMLQMEICIGFVFPFLIMGCVFTARTLMMKPNIKSRPLK 240
181 NARCIPPFRLGTSKMLQMEICIGFVFPFLIMGCVFTARTLMMKPNIKSRPLK 240
181 NARCIPPFRLGTSKMLQMEICIGFVFPFLIMGCVFTARTLMMKPNIKSRPLK 240
181 NARCIPPFRLGTSKMLQMEICIGFVFPFLIMGCVFTARTLMMKPNIKSRPLK 240
241 VLLTVVIVITVOLPYNTVKFCRAIDIYLSSITSCNMNSKRMIAIQVESIALFHSCLN 300
241 VLLTVVIVITVOLPYNTVKFCRAIDIYLSSITSCNMNSKRMIAIQVESIALFHSCLN 300
241 VLLTVVIVITVOLPYNTVKFCRAIDIYLSSITSCNMNSKRMIAIQVESIALFHSCLN 300
301 ILVYVGMASFKNYVMKVAKKGSWRQRQSVEEPESEGPREPTSTSI 350
RESULT 2
CKRB_BOVIN STANDARD PRT; 350 AA.
ID CKRB_BOVIN STANDARD PRT; 350 AA.
P35350; AC 1
DT 01-JUN-1994 (Rel. 29' created)
DT 01-JUN-1994 (Rel. 29, last annotation update)
DT 16-OCT-2001 (Rel. 40, last sequence update)
C-C chemokine receptor type 11 (C-C CKR-11) (CCR-11) (CCR-11)
DE (possible gustatory receptor type B) (PPRL protein).
CCRL1
GN CCR11
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
RN NCBI_TaxID=9513;
RN {1}
SEQUENCE FROM N_A.

RX TISSUE=tongue;
MEDLINE=93320166; PubMed=8392843;
MATSUOKA I.; MORI T.; AOKI J.; SATO T.; KURIHARA K.; RA
"Identification of novel members of G-protein coupled receptor
superfamily expressed in bovine taste tissue.";
RT Superfamily. Biochem. Biophys. Res. Commun. 194:504-511(1993).
RL Biochem. Biophys. Res. Commun. 194:504-511(1993).
CC -! FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4,
SCYA19/MIP3B/ELC, SCYA21/SAC AND SCYA5/TECK (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALVATE AND FUNIFORM
PAPILLAE; OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN
LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.
CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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or send an email to license@isb-sib.ch).
CC DR EMBL; S63848; AA27547; 1; -.
DR PIR; JN0621; JN0621.
DR HSSE; P02699; IBOJ.
DR InterPro; IPR002776; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS05062; G-PROTEIN RECEPTOR_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation.
FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 42 66 1 (POTENTIAL).
FT DOMAIN 67 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 99 2 (POTENTIAL).
FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 114 135 3 (POTENTIAL).
FT DOMAIN 136 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 175 4 (POTENTIAL).
FT DOMAIN 176 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 222 5 (POTENTIAL).
FT DOMAIN 223 241 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 242 265 6 (POTENTIAL).
FT DOMAIN 266 283 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284 306 7 (POTENTIAL).
FT DOMAIN 307 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 308 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 319 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 319 384 BY SIMILARITY.
SQ SEQUENCE 350 AA; 40008 MW; E46B942F3919C82 CRC64;
Query Match 89.1%; Score 1620; DB 1; Length 350;
Best Local Similarity 86.0%; Pred. No. 1.2e-91; O; Mismatches 27; Indels 0; Gaps 0;
Matches 301; Conservative 27; MisMatches 22; DR PROSITE; PS05062; G-PROTEIN RECEPTOR_F1_2; 1.
1 MALEQNSDSTYYEENEMGTYDSQEYELICKEDVREFAKVELPVLTIVFVLAGNS 60
1 MALEQNSDSTYYEENEMGTYDSQEYELICKEDVREFAKVELPVLTIVFVLAGNS 60
61 MVAIAYYKKRKRTDYTLNLAVADLFLTLPEWANAVHGWLKGKMRCKITSALYT 120
61 MVAIAYYKKRKRTDYTLNLAVADLFLTLPEWANAVHGWLKGKMRCKITSALYT 120
61 MVAIAYYKKRKRTDYTLNLAVADLFLTLPEWANAVHGWLKGKMRCKITSALYT 120
121 LNFGVSGMQLFACTISIDRVYAVTKVPSQSGVGKPCWICFCVWMAAIIISIPOLVFVYND 180
121 LNFGVSGMQLFACTISIDRVYAVTKVPSQSGVGKPCWICFCVWMAAIIISIPOLVFVYND 180
121 LNFGVSGMQLFACTISIDRVYAVTKVPSQSGVGKPCWICFCVWMAAIIISIPOLVFVYND 180
181 NARCIPPFRLGTSKMLQMEICIGFVFPFLIMGCVFTARTLMMKPNIKSRPLK 240
181 NARCIPPFRLGTSKMLQMEICIGFVFPFLIMGCVFTARTLMMKPNIKSRPLK 240
181 NARCIPPFRLGTSKMLQMEICIGFVFPFLIMGCVFTARTLMMKPNIKSRPLK 240
181 NARCIPPFRLGTSKMLQMEICIGFVFPFLIMGCVFTARTLMMKPNIKSRPLK 240

Query Match 35.1%; Score 639; DB 1; Length 369;
Best Local Similarity 36.0%; Pred. No. 2,7e-32; Mismatches 111; Indels 22; Gaps 5;
Matches 118; Conservatve 77; Mismatches 111; Indels 22; Gaps 5;
SEQUENCE 369 AA: 41913 MW: 6971F6F0A2B4AE CRC64;

QY 10 DYVYEE-NEMNGTY--DYSQVELICKEDVRKEAVLPFLTIVFVIGLAGNSMVAIY 66
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 16 DFSDFSTASTDDPMNLNFSSF--FCKKNRVRGEASHEPLPFLWLVFTGLNSVLIVY 73
QY 67 AYYKKQRTKDVTILNLAVIDLILLFTLPFWAVNAVHGWLKGIMCKITSALYTLMNVSG 126
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 74 WCYTRKVITMDMLNLLAIDLFLATLPFWATAIAAGOMMFOTFMCKVUNSNKMKNPSC 133
QY 127 MQLACISIDRYAVTKVPSOSGVGPKCW-----TICCVWMMAILSISPOLVFYT 177
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 134 VLLMCISDVRYIAVO---AMKAQWKRRLYLSKWCCTTIIWMAVLCPEIYSQ 188
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 178 VNNDN---ARCIPIPRYLGTSMKALIQMLEICGFVVPFLIMGVCYFTARTLKMNPNIK 234
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 189 VSGBSGGIACFTCMVTPKDKNAKLUKLAVLKVTLGFLPFMVWAFCYTTIHTLQAKSS 248
QY 235 ISRPKVLTIVTVFVTFQOLPYNIKVFKGRADITYSLTSNCNSKRMIDAIOWTESTALF 294
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 249 KHKALKVITVTVTFQIMSOFPYNSILVQAVDYMAMFISNCTISTNDICFOVQTIAFF 308
QY 295 HSCLNPLILVFMGASFKNYVMVKYAKYG 322
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 HSCLNPLILVFMGASFKNYVMVKYAKYG 322
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
SEQUENCE 357 AA: 40713 MW: 9692E0B22F6531 CRC64;

RESULT 6

CKR9_HUMAN	STANDARD:	PRT:	357 AA.
ID CKR9_HUMAN			
AC P51686;			
DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1996 (Rel. 34, last sequence update)			
DT 15-JUN-2002 (Rel. 41, last annotation update)			
DE C-C chemokine receptor type 9 (C-C CKR-9) (CCR-9) (GPR-9 - 6)			
GN CCR9 OR CMKBR9.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX NCBI_TAXID=9606;			
[1] RSEQUENCE FROM N.A.			
RA Lautens L.L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.N.,			
RA Bonner T.I.,			
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RR [2] CHARACTERIZATION.			
RX MEDLINE-99248139; PubMed-10229797;			
RA Zaballos A., Gutierrez J., Varona R., Ardevin C., Marquez G.; RT receptor for the orphan chemokine receptor GPR-9-6 as CCR9, the RL J. Immunol. 167:5671-5679.			
CC J. - FUNCTION: Receptor for chemokine SCYA25/TECK. Subsequently transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection.			

Query Match 35.0%; Score 637; DB 1; Length 357;
Best Local Similarity 36.5%; Pred. No. 3.4e-32; Mismatches 115; Indels 18; Gaps 4;
Matches 119; Conservatve 74; Mismatches 115; Indels 18; Gaps 4;
SEQUENCE 357 AA: 40713 MW: 9692E0B22F6531 CRC64;

QY 10 DYVYEE-NEMNGTYDYSQVELICKEDVRKEAVLPFLTIVFVIGLAGNSMVAIY 68
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 4 DYGSESTSSDMEDYVNFNFTDPYCEKNVRQDFASHPLPFLWLVFTGLNSVLIVY 63
QY 69 YRKQRTKDVTILNLAVIDLILLFTLPFWAVNAVHGWLKGIMCKITSALYTLMNVSG 128
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 CTRVKITMDMLNLLAIDLFLVLTLPFWATAIAAGOMMFOTFMCKVUNSNKMKNPSC 123
QY 129 FLACISIDRYAVTKVPSOSGVGPKCW-----TICCVWMMAILSISPOLVFYT 179
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 124 LIMCISDVRYIAVO---AMRAHTWREKRRLYLSKWCCTTIIWMAAICPEIYSQ 178
QY 180 DN---ARCIPIPRYLGTSMKALIQMLEICGFVVPFLIMGVCYFTARTLKMNPNIK 236
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 179 EBSGIACTMVPSDESTKPSAVLKVTLGFLPFMVWAFCYTTIHTLQAKSS 238
QY 237 RPLKVLTIVTVFVTFQIMSOFPYNSILVQAVDYMAMFISNCTISTNDICFOVQTIAFF 296
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 239 KALKVITVTVFVLSQFOPYNQNLVQTDAYAMFISNCAVSTNDICFOVQTIAFF 298
QY 297 CINPLIVFMGASFKNYVMVKYAKYG 322
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 299 CLNPVLIVFVGERFRRLDVKTLNLG 324

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
CC LYMPH NODES AND SPLEEN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to licensee@isb-sib.ch.)
DR -----
DR EMBL; U45982; AAA9319.1; -.
DR Genew; HGNC;1610; CCR9.
DR MM; 604738; -.
DR Interpro; IPR004069; CC_chemokine9.
DR Interpro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7m_1..1.
DR PRINTS; R01531; CHEMOKINER9.
DR PRINTS; PR0237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECCEP_F1_1; 1.
DR PROSITE; PS50562; G_PROTEIN_RECCEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 37
FT TRANSMEM 38 64
FT DOMAIN 65 73
FT TRANSMEM 74 94
FT DOMAIN 95 108
FT TRANSMEM 109 130
FT DOMAIN 131 148
FT TRANSMEM 169 4
FT DOMAIN 170 198
FT TRANSMEM 179 226
FT DOMAIN 227 242
FT TRANSMEM 243 268
FT DOMAIN 269 292
FT TRANSMEM 293 310
FT DOMAIN 311 357
FT CARBOHD 20 20
FT DISULFID 107 186
FT SEQUENCE 357 AA: 40713 MW: 9692E0B22F6531 CRC64;

Query Match 35.0%; Score 637; DB 1; Length 357;
Best Local Similarity 36.5%; Pred. No. 3.4e-32; Mismatches 115; Indels 18; Gaps 4;
Matches 119; Conservatve 74; Mismatches 115; Indels 18; Gaps 4;
SEQUENCE 357 AA: 40713 MW: 9692E0B22F6531 CRC64;

QY 10 DYVYEE-NEMNGTYDYSQVELICKEDVRKEAVLPFLTIVFVIGLAGNSMVAIY 68
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 4 DYGSESTSSDMEDYVNFNFTDPYCEKNVRQDFASHPLPFLWLVFTGLNSVLIVY 63
QY 69 YRKQRTKDVTILNLAVIDLILLFTLPFWAVNAVHGWLKGIMCKITSALYTLMNVSG 128
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 CTRVKITMDMLNLLAIDLFLVLTLPFWATAIAAGOMMFOTFMCKVUNSNKMKNPSC 123
QY 129 FLACISIDRYAVTKVPSOSGVGPKCW-----TICCVWMMAILSISPOLVFYT 179
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 124 LIMCISDVRYIAVO---AMRAHTWREKRRLYLSKWCCTTIIWMAAICPEIYSQ 178
QY 180 DN---ARCIPIPRYLGTSMKALIQMLEICGFVVPFLIMGVCYFTARTLKMNPNIK 236
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 179 EBSGIACTMVPSDESTKPSAVLKVTLGFLPFMVWAFCYTTIHTLQAKSS 238
QY 237 RPLKVLTIVTVFVTFQIMSOFPYNSILVQAVDYMAMFISNCTISTNDICFOVQTIAFF 296
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 239 KALKVITVTVFVLSQFOPYNQNLVQTDAYAMFISNCAVSTNDICFOVQTIAFF 298
QY 297 CINPLIVFMGASFKNYVMVKYAKYG 322
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 299 CLNPVLIVFVGERFRRLDVKTLNLG 324

		Matches	Conservative	Mismatches	Indels	Gaps
CKR6_MOUSE	STANDARD;	PRT; 367 AA.				
ID CKR6_MOUSE						
AC 054889;						
DT 30-MAY-2000 (Rel. 39, Created)						
DT 30-MAY-2000 (Rel. 39, Last sequence update)						
DT 30-OCT-2001 (Rel. 40, Last annotation update)						
DE C-C chemokine receptor type 6 (C-C CKR-6) (CCR-6) (KY411).						
CCR6 OR CMKBR6.						
OS Mus musculus (Mouse).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX NCBI_TaxID=10090;						
RN [1]						
RP SEQUENCE FROM N.A.						
RA Yanagihara S., Konura E., Yanaguchi Y.;						
RA "Mouse G Protein-coupled receptor KY411."						
RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.						
RN [2]						
RP SEQUENCE FROM N.A.						
RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F., Alvar J.P., Ardevin C., Marquez G.;						
RT "Molecular cloning, functional characterization and mRNA expression analysis of the murine chemokine receptor CCR6 and its specific ligand MIP-3alpha."; EBBS Lett. 440:188-194(1998).						
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-						
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE						
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.						
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.						
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CC EMBL; AD009369; BRA23776.1; -.						
CC DR MGD; MG:1333797; CMKBR6.						
DR InterPro; IPR004067; CC_chemokine6.						
DR PFam; PF00001; Tm_1.; 1.						
DR PRINTS; PR01529; CHEMOKINERG.						
DR PROSITE; PRO0237; GPCRRIODPSN.						
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_1.; 1.						
KW G-Protein coupled receptor; Transmembrane; Glycoprotein.						
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).						
FT TRANSMEM 40 66 CYTOPLASMIC (POTENTIAL).						
FT DOMAIN 67 75 2 (POTENTIAL).						
FT TRANSMEM 76 96 2 (POTENTIAL).						
FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).						
FT TRANSMEM 112 133 3 (POTENTIAL).						
FT DOMAIN 134 151 CYTOPLASMIC (POTENTIAL).						
FT TRANSMEM 152 172 4 (POTENTIAL).						
FT DOMAIN 173 203 EXTRACELLULAR (POTENTIAL).						
FT TRANSMEM 204 230 5 (POTENTIAL).						
FT DOMAIN 231 246 CYTOPLASMIC (POTENTIAL).						
FT TRANSMEM 247 271 6 (POTENTIAL).						
FT DOMAIN 272 295 EXTRACELLULAR (POTENTIAL).						
FT TRANSMEM 296 313 7 (POTENTIAL).						
FT DOMAIN 314 367 CYTOPLASMIC (POTENTIAL).						
FT DISULFO 110 189 BY SIMILARITY.						
FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).						
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).						
SQ SEQUENCE 367 AA; 42102 MW; 6A309AF83B117E CRC64;						
Query Match Best Local Similarity 33.3%; Score 605; Pred. No. 3e-30; Length 367;						
RL						
RESULT 8						
CKR6_HUMAN						
ID CKR6_HUMAN						
AC P51684; Q02846; P79553;						
DT 01-OCT-1995 (Rel. 34, Created)						
DT 15-JUL-1998 (Rel. 36, Last sequence update)						
DT 16-OCT-2001 (Rel. 40, Last annotation update)						
DE C-C chemokine receptor type 6 (C-C CKR-6) (CCR-6) (LARC receptor) (GPR-CY4) (GPR6) (Chemokine receptor-like 3) (CKR-L3) (DRY6).						
DE CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.						
OS Homo sapiens (Human).						
OC Bukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX NCBI_TaxID=9605;						
RN [1]						
RP SEQUENCE FROM N.A., AND FUNCTION.						
RA MEDLINE=9731465; Pubmed=9159459;						
RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K., Nomiyama H., Yoshie O.;						
RT "Identification of CCR6, the specific receptor for a novel lymphocyte-directed CC chemokine LARC"; J. Biol. Chem. 272:14893-14898(1997).						
RL [2]						
SEQUENCE FROM N.A.						
Lautens L.-I., Modi W., Bonner T.I.; [3] Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.						
RP SEQUENCE FROM N.A.						
RA MEDLINE=97040707; Pubmed=8886020;						
RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.; McCoy R., Perlmutter D.H.;						
RT Molecular cloning and RNA expression of two new human chemokine receptor-like genes"; Biophys. Res. Commun. 227:846-853(1996).						
RL Biochem. Biophys. Res. Commun. 227:846-853(1996).						
RA SEQUENCE FROM N.A.						
RA MEDLINE=97224503; Pubmed=9070937;						
RA Liao F., Lee H.-H., Farber J.M.;						
RT "Cloning of SRL22, a new human gene encoding a G-protein-coupled receptor related to chemokine receptors and located on chromosome 6q27." Genomics 40:175-180(1997).						
RL						

!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3⁻
 ALPHAYLARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 INTRACELLULAR CALCIUM IONS LEVEL.
 !- SUBCELLULAR LOCATION: Integral membrane protein.
 !- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
 LIVER. EXPRESSED IN LYMPHOcytes, T CELLS AND B CELLS BUT NOT IN
 NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCytes.
 !- INDUCTION: BY INTERLEUKIN-2.
 !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPtoRs.
 !- CAUTION: IT IS UNcERTAIN WHETHER MIP-1 OR MIP-6 IS THE INITIATOR.

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CC QY 68 YIKKQRTKDVILVNLAVADLLFLTPFWAY-NAVHGWWGKIMCKITSALYTLNFVSG 126
 CC :||| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 CC FT 73 FYKKARSMTDVLLNMAIDILFVLPLPFWASHATGAWNSNACKLGIVAINFNCG 132
 CC QY 127 MOFLACISIDRYAVATKVPS---QSGVGPWCITFCVWMAAILLISIPOUVE--YTVN 179
 CC :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 CC DB 133 MLITCISMMDRVIAVQATKSFRRLRSRTLPRSKICLUVWGLSVISSLSTFVNQINTO 192
 CC QY 180 DNARCIPIPPRLGTS---MKALIQMLECIGFVVPFLNGVCFTARTLMKPNIKI 235
 CC :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 CC DB 193 GSIVC---EPKIQTVSPRIRWLMLGFLRFPFLPMFMPCVYFIVKNTWQONSKR 249
 CC :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 DR QY 236 SRPLKVLTIVVIFVQPLPVNPKCRAIDIYSLITSCNMNSKRMDIAQTESIAFLH 295
 DR :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 DR DB 250 HKAIRVITAVIAVWLFQDQPHNMVLVTAAN-LGKUNRSCOSEKLGIFTKVTEVLAFLH 308
 DR QY 296 SCINPLIVVEMGASFKNVWVAKKGWSWRQRQS 330
 DR :|||:|||:|||:|||:|||:|||:|||:
 DR DB 309 CCLNPVLYAFIGOKFRNYFLKILKDLWCVRRKYS 343

RESULT 9
 ID CCR6_CERAE
 ID CCR6_CERAE STANDARD: PRT: 342 AA.

ID 018983; DE [1]

ID 15-JUL-1998 (Rel. 36, Created)

ID 15-JUL-1998 (Rel. 36, Last sequence update)

ID 15-JUN-2002 (Rel. 41, Last annotation update)

ID C-X-C chemokine receptor type 6 (CXC-R6) (CXCR-6) (G protein-coupled receptor bonzo).

ID CXCR6 OR RONZO.

ID GN

ID OX Cercopithecus aethiops (Green monkey) (Grivet).

ID OC Mammalia; Eutheria; Primates; Catarrini; Cercopithecidae;

ID OC Cercopithecinae; Cercopithecus.

ID RN [1]

ID RP SEQUENCE FROM N.A.

ID RX MEDLINE=9733958; PubMed=9230441;

ID RA Deng H-K., Unutmaz D., Kewalramani V.N., Litman D.R.;

ID RT "Expression cloning of new receptors used by simian and human immunodeficiency viruses.";

ID RL Nature 388:296-300(1997).

ID CC -1 FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A CORRECEPTOR BY SIVs AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.

ID CC -1 SUBCELLULAR LOCATION: Integral membrane protein.

ID CC -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPtoRs.

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CC DR PROSITE: PS00237; GPCR_Rhodpsn.

DR EMBL: AE007859; AB64225.1; -

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pram: PR00001; 7tm.1; 1.

DR PRINS: PRO0237; GPCR_Rhodpsn.

DR PROSITE: PS00262; G_protein_recceptor_FL1_2; 1.

DR KW G_protein_coupled_receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 33 59 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 60 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 90 103 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 104 125 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 126 143 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 144 164 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 165 187 EXTRACELLULAR (POTENTIAL).

Query Match Best Local Similarity Score: 32.18; Length: 374;
 Matches: 121; Conservative: 36.1%; Pred. No.: 6.6e-29;
 Qy 8 STDYYEEENERGTYDYSQYELCITEDREKFAYKFLPVFLTVFVIGAGNSMVATYA 67
 Db 23 NTSYKVDSEM-----LCLSQEVRQFSRDFVPAISLICVFGLGNLWVTF 72

FT	TRANSMEM	144	164	4 (POTENTIAL).	RN	[3]
FT	DOMAIN	165	187	EXTRACELLULAR (POTENTIAL).	RP	FUNCTION:
FT	TRANSMEM	188	215	5 (POTENTIAL).	RX	MEDLINE:97313486; PubMed=9169480;
FT	DOMAIN	216	231	CYTOPLASMIC (POTENTIAL).	RA	Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshiie O.;
FT	TRANSMEM	232	259	6 (POTENTIAL).	RT	"The T cell-directed CC chemokine TARC is a highly specific
FT	DOMAIN	260	275	EXTRACELLULAR (POTENTIAL).	RT	biological ligand for CC chemokine receptor 4";
FT	TRANSMEM	276	293	7 (POTENTIAL).	RL	J. Biol. Chem. 272:15036-15042(1997);
FT	DOMAIN	294	342	CYTOSPLIC (POTENTIAL).	RN	[4]
FT	DISULFID	102	180	BY SIMILARITY.	RP	FUNCTION:
FT	CARBONYL	16	16	N-LINKED (GLCNAC. . .) (POTENTIAL).	RX	MEDLINE:98104168; PubMed=9430724;
FT	VARIANT	25	25	D -> A (IN STR33.3).	RA	Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
SQ	SEQUENCE	342 AA:	39280 MW:	/FTID=VAR 003506;	RA	"Macrophage-derived chemokine is a functional ligand for the CC
Query Match		30.8%	Score 560; DB 1; Length 342;		RT	Yoshiie O., Gray P.W.;
Best Local Similarity		33.1%	Pred. No. 1.5e-27;		RT	Chemokine receptor 4.;
Matches	117;	Conservative	75; Mismatches 130; Indels 32; Gaps 8;		RL	J. Biol. Chem. 273:1764-1768(1998);
Oy	12	YVEENEMGTYDQSYLELICKEDREFARAVFLPVLFVLTIVFUGLAGNSMVAYAYKK	71		RN	[5]
Oy	132	CISIDRVYAVATKVP-----QSGVGKPCW---ITCFCCWMATILLSPOLVFTV-NDNARCI	185		FUNCTION:	
Oy	122	YHEDYGFSSFNDSBEE---HODLQFSKVRFLCPMLYVPCGIVLGVNSLVLVISIFHK	61		RX	MEDLINE:99394604; PubMed=10466728;
Oy	72	QFTKTDVYILNLAVADLLTLPWAVNAVHGWGLKGIMCKTSALYLNFPSGMFLA	131		RA	Campbell J.J., Haraldsen G., Pan J., Rottman J., Olin S., Ponath P.,
Oy	62	62 LQSLTDYFLVNLPLADLVFLVPLFWAYACTHENWFGQVMCKSILGIVTINFYTSMLLT	245		RA	Andrew D.P., Warne R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
Db	181	--GHDDEAISTSVVLAQTMQTLGGFLPLLTIVCYSVITLHLAGGEOKHRSLKILFV	236		RT	"The chemokine receptor CC4 in vascular recognition by cutaneous but
Oy	246	132 CIVTVDRFLIVVVKATRAYNQAKRMWGVYVLSLWISLVSQIQLYGNVNFDKLIC-	180		RT	not intestinal memory T cells.;"
Db	237	237 MAVFLLTOMPNLKFIRSTHWEYAMTSFY-----IMVTEAIYRACLNPVLA	290		RL	Nature 400:776-780(1999);
Oy	186	186 PRFPRLGTGTSKAKLQMLCIGFVPUFLINGVCYFITAATLKMNPNTKISRPKVLY	245		RP	[6]
Db	181	--GHDDEAISTSVVLAQTMQTLGGFLPLLTIVCYSVITLHLAGGEOKHRSLKILFV	236		RX	FUNCTION: TISSUE SPECIFICITY AND PHOSPHORYLATION.
Oy	306	306 MGASFNNYVMKVAKKYG-----SWRRQRQSVEEPFDSEGPTEPTSTFSI	350		RA	MEDLINE:20219338; PubMed=10754297;
Oy	291	291 VSLKERKKNFKLVDIGCLYLYGVSHQWSSESDNSK-TFSASHINVEATSMFQL	342		RA	Langjercigen M., Damaj B., Magnazachi A.A.;
CC	RESULTS	13			CC	"Human NK cells express CC chemokine receptors 4 and 8 and respond to
CCR4_HUMAN	ID	CCKR4_HUMAN	STANDARD;	PRT;	CC	HOMING RECEPTOR ON CIRCULATING MEMORY LYMPHOCTYES AND AS A
AC	PR01679; 09UYL6; 09UYL7;			360 AA.	CC	CORECEPTOR FOR SOME PRIMARY HIV-2 ISOLATES. IN THE CNS, COULD
DT	01-OCT-1996 (Rel. 34, Created)				CC	MEDIATE HIV-2 ISOLATES. IN THE CNS, COULD
DT	01-OCT-1996 (Rel. 34, Last sequence update)				CC	-I FUNCTION: HIGH AFFINITY RECEPTOR FOR THE C-C TYPE CHEMOKINES
DE	16-OCT-2001 (Rel. 40, Last annotation update)				CC	TARC/SCYA17 AND MDC/SCYA22. THE ACTIVITY OF THIS RECEPTOR IS
DE	C-C chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR4)				CC	MEDIATED BY G(T) PROTEINS WHICH ACTIVATE A PROSHPATIDYLINOSITOL-
GN	CCR4 OR CMBR4.				CC	CALCIUM SECOND MESSENGER SYSTEM. CAN FUNCTION AS A CHEMOATTRACTANT
OS	Homo sapiens (Human).				CC	HOMING RECEPTOR ON CIRCULATING MEMORY LYMPHOCTYES AND AS A
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				CC	CORECEPTOR FOR SOME PRIMARY HIV-2 ISOLATES. IN THE CNS, COULD
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				CC	MEDIATE HIV-2 ISOLATES. IN THE CNS, COULD
NCBI_TAXID=9606;					CC	-I TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE THYMUS, IN
[1]	SEQUENCE FROM N_A.				CC	PERIPHERAL BLOOD LEUKOCYTES, INCLUDING T CELLS, MOSTLY CD4+ CELLS,
RC	TISSUE=Spleen;				CC	AND IN MONOCYTES. DETECTED ALSO IN MACROPHAGES, IL-2-ACTIVATED
RX	MEDLINE=95370269; PubMed=642634;				CC	NATURAL KILLER CELLS AND SKIN-HOMING MEMORY T CELLS, MOSTLY THE
RA	Power C.A., Meyer K., Nemeth K., Bacon K.B., Hoogewerf A.J.,				CC	ONES EXPRESSING THE CUTANEOUS LYMPHOCITE ANTIGEN (CLA). EXPRESSED
RA	Proudfoot A.E.T., Wells T.N.C.;				CC	IN BRAIN MICROVASCULAR AND CORONARY ARTERY ENDOTHELIAL CELLS.
RT	"Molecular cloning and functional expression of a novel CC chemokine				CC	-!- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
RT	receptor cDNA from a human basophilic cell line.",				CC	PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
RL	J. Biol. Chem. 270:19495-19500(1995).				CC	BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.
RN	{12}	SEQUENCE FROM N_A., AND VARIANTS VAL-130 AND SER-178.			CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
RP	SEQUENCE FROM N_A., AND VARIANTS VAL-130 AND SER-178.				CC	-----
RP	INTERPRO: IPR002276; GPCR_Rhodopsin.				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RX	MEDLINE=21040311; PubMed=1116669;				CC	between the Swiss Institute of Bioinformatics and the EMBL database. There are no restrictions on its
RA	Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,				CC	use by non-profit institutions as long as its content is in no way
RA	Hirai K., Tokunaga K.;				CC	modified and this statement is not removed. Usage by and for commercial
RA	"New variations of human CC-chemokine receptors CCR3 and CCR4.,"				CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
RN	Genes Immun. 1:97-104(1999).				CC	or send an email to license@isb-sib.ch).
RP	SEQUENCE FROM N_A.				CC	-----
RC	SEQUENCE FROM N_A.				CC	-----
RX	SEQUENCE FROM N_A., AND VARIANTS VAL-130 AND SER-178.				CC	-----
RA	INTERPRO: IPR002276; GPCR_Rhodopsin.				CC	-----
RA	MEDLINE=21040311; PubMed=1116669;				CC	-----
RA	Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,				CC	-----
RA	Hirai K., Tokunaga K.;				CC	-----
RA	"New variations of human CC-chemokine receptors CCR3 and CCR4.,"				CC	-----
RN	Genes Immun. 1:97-104(1999).				CC	-----

PT	Phosphorylation; Polymorphism.
FT DOMAIN	1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	40 67 (POTENTIAL).
FT DOMAIN	68 77 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	78 98 2 (POTENTIAL).
FT DOMAIN	99 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	112 133 3 (POTENTIAL).
FT DOMAIN	134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	151 175 4 (POTENTIAL).
FT DOMAIN	176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	207 226 5 (POTENTIAL).
FT DOMAIN	227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	243 267 6 (POTENTIAL).
FT DOMAIN	268 284 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	285 308 7 (POTENTIAL).
FT DOMAIN	309 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD	183 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID	110 187 BY SIMILARITY.
FT VARIANT	130 130 L -> V.
FT VARIANT	178 178 /FTid=VAR_010670.
FT	SEQUENCE FROM N.A.
FT	RC MEDLINE=94209213; PubMed=7512557;
FT	RX TISSUE=Placenta;
FT	RA MEDLINE=95014476; PubMed=7929358;
FT	RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
FT	RT "Structure, genomic organization, and expression of the human
FT	RT Interleukin-8 receptor B gene;"
FT	RL Mol. Immunol. 30:359-367(1993).
FT	RN [3]
FT	RP SEQUENCE FROM N.A.
FT	RC MEDLINE=94209213; PubMed=7512557;
FT	RX TISSUE=Placenta;
FT	RA MEDLINE=95014476; PubMed=7929358;
FT	RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
FT	RT "Comparison of the genomic organization and promoter function for
FT	RT human interleukin 8 receptors A and B.,"
FT	RL J. Biol. Chem. 269:26381-26389(1994).
FT	RN [5]
FT	RP CHARACTERIZATION.
FT	RA MEDLINE=93355587; PubMed=1379593;
FT	RA Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
FT	RT "Characterization of two high affinity human interleukin-8 receptors";
FT	RL J. Biol. Chem. 267:16283-16287(1992).
FT	CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8 WHICH IS A POWERFUL
FT	CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
FT	CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
FT	CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
FT	CC MESSENGER SYSTEM. THIS RECEPTOR Binds TO IL-8 WITH A HIGH AFFINITY
FT	CC AND TO GR018A AND NAP-2 ALSO WITH A HIGH AFFINITY.
FT	CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
FT	CC -- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FT	CC -- DATABASE: NAME=PROW; NOTE=CD guide Cdw12Bb entry;
FT	CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw12Bb.htm".
FT	CC -----
FT	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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FT	CC -----
FT	DR EMBL; M7369; AAA83148.1; -.
FT	DR EMBL; M9482; AAA36108.1; -.
FT	DR EMBL; M9912; AAC1460.1; -.
FT	DR EMBL; M9912; AAC1460.1; -.
FT	DR EMBL; M9482; AAA36108.1; -.
FT	DR EMBL; M9912; AAC1460.1; -.
FT	DR EMBL; L19593; KAB5943.1; -.
FT	DR EMBL; U11669; BAB60556.1; -.
FT	DR PIR; A3946; A3946.
FT	DR PIR; A53611; A53611.
FT	DR HSSP; P34596; IDDD.
FT	DR Gene; HGNC:6027; IL8RB.
FT	DR MIM: 146958; -.
FT	DR InterPro; IPR00276; GPCR_Rhodopsin.
FT	DR InterPro; IPR00832; GPCR_secretin.
FT	DR Pfam; PF00001; 7tm_1..1.
FT	DR PRINTS; PR00237; GPERRHODOPSIN.
FT	DR PROSITE; PS50562; G-PROTEIN_RECEP_FL1; 1.
FT	DR KW PROSITE; PS50562; G-PROTEIN_RECEP_FL2; 1.
FT	DR KW G-protein coupled receptor; Transmembrane; Glycoprotein;
FT	FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
FT	FT DOMAIN 49 75 1 (POTENTIAL).
FT	FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).

Query Match 29, 4%; Score 534.5; DB 1; Length 360;
 Best Local Similarity 33.2%; Pred. No. 5.5e-26; Mismatches 75; Indels 25; Gaps 8;
 Matches 120; Conservative 75; N-LINKED (GLCNAC. . .) (POTENTIAL).
 BY SIMILARITY.

Qy 3 LEQNOSTDYYIYEEENEMGTYDYSQVELI---CIKEDVREFAKVFLPVFTIVFVIGLA 57
 Db 6 MESDSFDFWKGEDLSNSY\$STLPFLDAACPEPSL-EINKYFVWVLIYAVFLSSL 64

CC CC MESSANGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MOSA AND NAF-2 ALSO WITH A HIGH AFFINITY.
 CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

FT DOMAIN 106 120 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 164 183 4 (POTENTIAL).
 FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 231 5 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 232 251 6 (POTENTIAL).
 FT TRANSMEM 252 273 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 274 294 7 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 295 315
 FT DOMAIN 316 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 22 22 BY SIMILARITY.
 FT DISULFID 119 196 SQ SEQUENCE 360 AA; 40759 MW; 584F04R8BCC0197 CRC64;

Query Match 29, 4%; Score 534.5; DB 1; Length 360;
 Best Local Similarity 33.2%; Pred. No. 5.5e-26; Mismatches 75; Indels 25; Gaps 8;
 Matches 120; Conservative 75; N-LINKED (GLCNAC. . .) (POTENTIAL).
 BY SIMILARITY.

Qy 3 LEQNOSTDYYIYEEENEMGTYDYSQVELI---CIKEDVREFAKVFLPVFTIVFVIGLA 57
 Db 6 MESDSFDFWKGEDLSNSY\$STLPFLDAACPEPSL-EINKYFVWVLIYAVFLSSL 64

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DR EMBL; X91113; CA62563.1; -.
 DR HSPP; P34996; IIDD.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR000332; GPCR_Secretin.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F2_1.
 DR G_protein_coupled_receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN <1 45 NON-TER 1
 FT TRANSMEM 46 72 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 81 81 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 82 102 2 (POTENTIAL).
 FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 118 139 3 (POTENTIAL).
 FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 180 4 (POTENTIAL).
 FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 228 5 (POTENTIAL).
 FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 249 270 6 (POTENTIAL).
 FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 292 312 7 (POTENTIAL).
 FT DOMAIN 313 >53 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 119 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON-TER 353 353 SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;

Query Match 29, 1%; Score 529.5; DB 1; Length 353;
 Best Local Similarity 33.6%; Pred. No. 1.1e-25; Mismatches 74; Indels 27; Gaps 8;
 Matches 118; Conservative 74; N-LINKED (GLCNAC. . .) (POTENTIAL).
 BY SIMILARITY.

Qy 3 LEQNOSTDYYIYEEENEMGTYDYSQVELI---CIKEDVREFAKVFLPVFTIVFVIGLA 57
 Db 3 MESDSFDFWKGEDLSNSY\$STLPFLDAACPEPSL-EINKYFVWVLIYAVFLSSL 61

CC CC RESULT 1.5
 ID IL8B_PANTR STANDARD; PRT; 353 AA.
 AC Q28807; 35', created)
 DT 01-Nov-1997 (Rel. 35, last sequence update)
 DT 01-Nov-1997 (Rel. 35, last annotation update)
 DE High affinity interleukin-8 receptor B (IL-8R B) (Fragment).
 GN IL8RB OR CXCR2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
 OX NCBI_TaxID=598;
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed=9110929;
 RP MEDLINE=9617515;
 RX Alvarez V., Coto F., Setien F., Gonzalez S., Gonzalez-Roces S., Lopez-Larrea C.;
 RT Characterization of interleukin-8 receptors in non-human primates.;
 RL Immunogenetics 43:261-267(1996).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 NEUTROPHIL CHONTOACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND

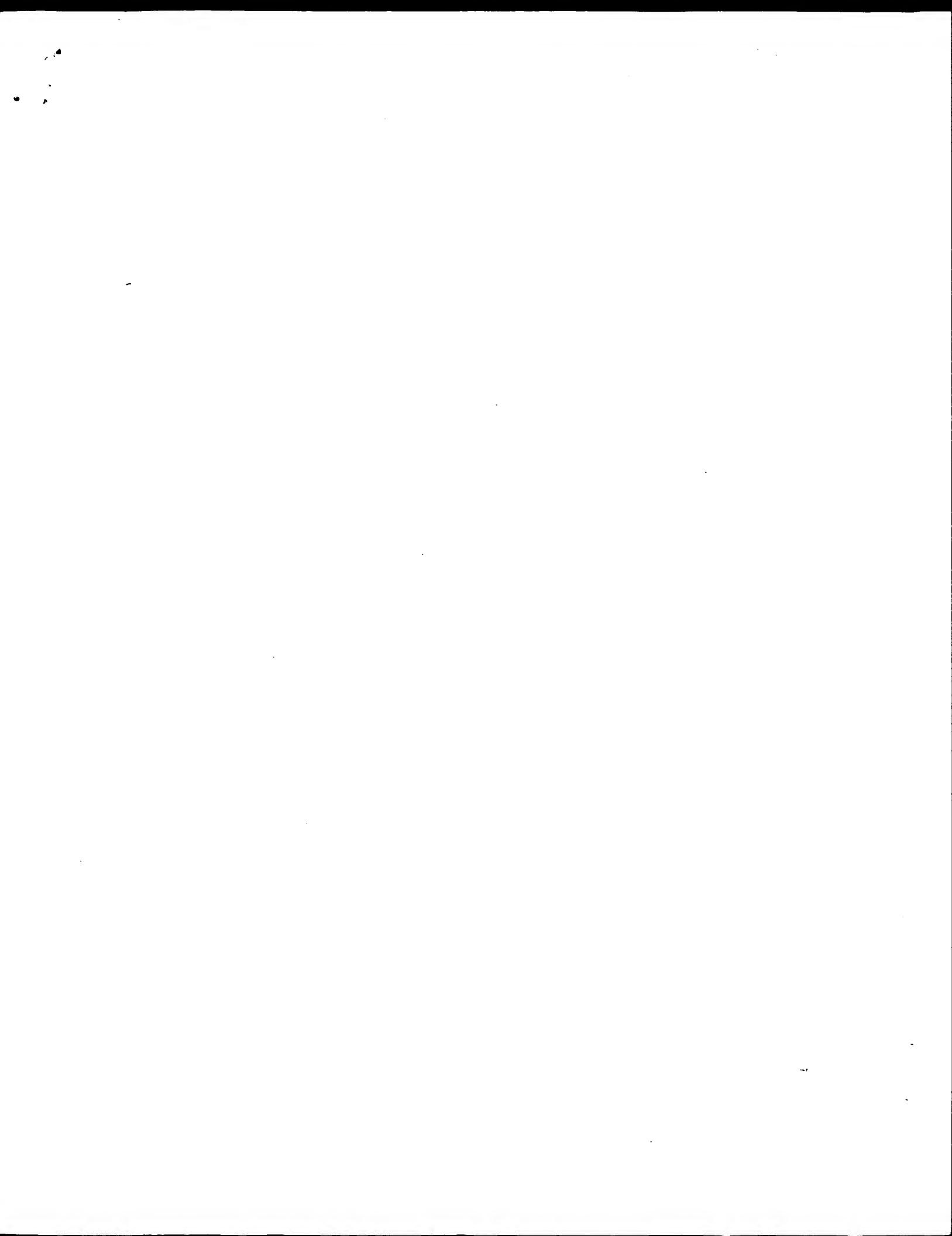
Search completed: March 14, 2003, 16:11:45

Mon Mar 17 12:24:55 2003

us-09-686-020a-2.rsp

Page 13

Job time : 13 secs



OM protein - protein search, using sw model	Ran on:	March 14, 2003, 16:10:47 ; Search time 19 Seconds (without alignments)		
Sequence:	I MALEQNQSTDYYBENEMNG VEEFPFDSEGPNTPTSTFSI 350	1770.897 Million cell updates/sec		
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5		
Searched:	283224 seqs, 93134422 residues			
total number of hits satisfying chosen parameters:	283224			
Minimum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing:	Minimum Match 0%			
Database :	Maximum Match 100%			
	Listing first 45 summaries			
		SUMMARIES		
Result No.	Score	Query Length	DB ID	Description
1	1620	89.1	JN0621	G protein-coupled receptor type B - bovine
2	659	36.2	B55735	C;Species: Bos primigenius taurus (cattle)
3	650	35.7	A55735	C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
4	643	35.3	A55680	C;Accession: JN0621 ; R:Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K. ; Biochem. Biophys. Res. Commun. 194, 504-511, 1993
5	583	32.1	JC5068	A;Title: Identification of novel members of G-protein coupled receptor superfamily expressed in rat brain
6	537.5	29.5	A57160	A;Reference number: JN0621; MID:9326166; PMID:8392843
7	534.5	29.4	A53611	A;Accession: JN0621
8	524	28.8	I50186	A;Molecule type: mRNA
9	522.5	28.7	JC4304	A;Residues: 1-350 <MAT>
10	522.5	28.7	AA5487	A;Cross-references: GB:SG3848; NID:9399710; PIDN:AAB27547.1; PID:9399711
11	518.5	28.5	JC5068	A;Experimental source: tongue taste papillae
12	511	28.1	A55752	C;Comment: This Protein is involved in modulating taste sensitivity or regeneration capacity
13	501.5	27.5	JQ1231	C;Superfamily: vertebrate rhodopsin
14	500.5	27.5	A45747	C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
15	499.5	27.5	S20787	F:42-66/Domain: transmembrane #status predicted
16	493.5	27.1	G00048	F:80-99/Domain: transmembrane #status predicted
17	492	27.0	JC2443	F:154-175/Domain: transmembrane #status predicted
18	489.5	26.9	A59445	F:200-222/Domain: transmembrane #status predicted
19	486	26.7	JG5067	F:242-265/Domain: transmembrane #status predicted
20	485	26.7	I49339	F:284-306/Domain: transmembrane #status predicted
21	484.5	26.6	A43113	F:6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted
22	483.5	26.6	A48921	Query Match 89.1%; Score 1620; DB 2; Length 350; Best Local Similarity 86.0%; Pred. No. 1. 3.e-131; Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;
23	482	26.5	JT8450	Db 1 MALEQNQSTDYYBENEMNGDYSQELICIVRKEVFLVFLTVFVLAGNS 60
24	479.5	26.4	J49341	Db 1 MAVCPFPLGTSKAKTQILECIGFVVFPLIMGVCFYITARTMLKPNIKTSRPLK 240
25	476.5	26.2	JE0349	Db 121 VNFSQGMQLACTSDPRYWAVTAKPSQSGVKPCWIVCFVWAAILSPOLFYTVND 180
26	474	26.1	A45177	Db 61 TVVATVAYKKRKRTKTDVYLNLAVADLFLLFTLPFWAVNAVHGWLKGKIMKVTSALYT 120
27	471	25.9	S20296	Qy 121 NARCIPIPRYLGSKMKALIOTLCITGFVVFPLIMGVCFYITARTMLKPNIKTSRPLK 240
28	470	25.8	S55594	Db 181 KARCPVIFPFLGTSKAKTQILECIGFVVFPLIMGVCFYITARTMLKPNIKTSRPLK 240
29	461.5	25.4	JO2436	Db 121 VNFVSGMQMFLACTSDPRYWAVTAKPSQSGVKPCWIVCFVWAAILSPOLFYTVNH 180
			Qy 241 VLTWVVFVTOVLQPYNIVFCRAIDIYSLITSNCNMKRMDIAQTQESIALEFHSCINP 300	
			Db 241 VLFTWVVFVTOVLQPYNIVFCQADIDYSLITSNCNMKRMDIAQTQESIALEFHSCINP 300	
			Qy 301 ILYVENGASFKVYMKVAKYGSWRQRQSOVEFFPDSQEPTEPTSTFSI 350	

Db 301 VLYVFMGTSKKNYIMKAVAKKGNSRQRONVEREIPPFESEDATEPPTSTFSI 350
RESULT 2
B55735 Lymphocyte-specific G protein-coupled receptor EBI1 - human
N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
A;Accession: B55735; S52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31580; NID:9468340; PIDN:AAA74232.1; PID:9468340
R;Burgstahler, R.; Kempkes, B.; Staebue, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A;Description: The expression of the chemokine receptor BUR2/EBI1 is specifically trans
A;Reference number: S52443
A;Accession: S52443
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <BUR>
A;Map position: 17q21-17q21.2
A;Cross-references: EMBL:X84702
C;Genetics:
A;Gene: GDB:C0KBR7; EBI1; BLR2; CCR7
A;Cross-references: GDB:342065; OMIM:600242
A;Map position: 17q21-17q21.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
Query Match 36.2%; Score 659; DB 2; Length 378;
Best Local Similarity 38.7%; Pred. No. 4.8e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
Qy 1 MALEQNQSTDYYENEMNGTYDSQEYELICKIKDVKDREPAKEVLPFLVTFWVGLAGNSMVA. 64
Db 21 VLCQDEDEVTDYIGDT--TVDYTLFESLCSKDKVRNFKAWEFLPIMSLICFVGILING 77
Qy 61 MWVAYIAYKKKQRKTDVYLNLAVADILFLPFWAVNAVTHGWGVGKIMOKKITSALYT 120
Db 78 LVVLYTYIFKRLKTMDTFLNLAVADILFLPFWAVWAASKSWWFGVHFCKLIAFYK 137
Qy 121 LNFTSGMQFLACISIDRVVAVTIVPS---OSGVGPCKWILCFCVWAAILSIPQIVY 176
Db 138 MSFPGMLLILCISIDRVVAVTIVPS---OSGVGPCKWILCFCVWAAILSIPQIVY 197
Qy 177 TVNDNA----ROPIPIFRYLGTSMKALIQMLCIGVFPVFLIMGVCYFTPARTLMP 231
Db 198 DIQRSSEAMRQLSITH--WEAFTIQVQAMWFLVPLIAMSFCYLWIRTLQAR 254
Qy 232 NTIKISRPKVLTVWIVFLVTOQPYNIVKFCRADILYSLITSCNMNSKRMDIAIQTESI 291
Db 255 NFERNAKIVIILAVVWVFLVQAOVWNFNTTSCLSKQLNIAYDVYSL 314
Qy 292 ALPHSCLNPLVFMGASFKNVKAKKG ---SW---RRQROSPEPFD 337
Db 315 ACYRCCVNFLVAFQIVKFRNDLFKFLRDGLSISOEQRLQWSSCRHRRSSMSVE--- 369
Qy 338 SEGPTEPMSTFS 349
Db 370 ---AEITTFS 377
RESULT 4
A45680 G protein-coupled peptide receptor EBI 1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
A;Accession: A45680
R;Birkenbach, M.; Josefsson, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled
A;Reference number: A45680; MUID:93188173; PMID:8383238
A;Accession: A45680
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-378 <GB>
A;Cross-references: B-lymphocytes
A;Experimental source: NCBP1 backbone (NCBIN:127094, NCBP1:127095)
A;Note: sequence extracted from NCBP1 backbone (NCBIN:127094, NCBP1:127095)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
Query Match 35.3%; Score 643; DB 2; Length 378;
Best Local Similarity 39.0%; Pred. No. 1.1e-47;
Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;
Qy 1 MALEQNQSTDYYENEMNGTYDSQEYELICKIKDVKDREPAKEVLPFLVTFWVGLAGNS 60
C;Species: Mus musculus (house mouse)

RESULT 3
A55735 G protein-coupled receptor EBI1 - mouse

Db 21 VCLCODEVTDYIGDT---TVDTLFESLCSKKVRNEKAWITIPIMSIICFVGGLNG 77
 Qy 61 MVAIAYAYIKKQRKTDVYLNLAVALDILFLPFWAVNAVAGWLGKIMCITSALY 120
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 78 LIVLVLYIYFRKLTKMTDYLNLAVALDILFLPFWAVSAAKSWVFGVHCKLIFAIYK 137
 Qy 121 LNIVSGCMQFLACISDRYAVTKVPSQSGVGPWII--CFCWMA--AIIISPOLFY 176
 ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 138 MSFFSGMLLICISIDYRAVQSAHRRAVYLILSKLSCYGSATLAVISPELLYS 197
 Qy 177 TNDNA----RCPIPRVLGTSKALIQMLEICIGFVPPFLIMGVCFITARTLMKMP 231
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 198 DLQRSSSEQAMRCSLITEH---VEAFITQVOAQMVGFLVPLAMSFCYLVIRTLLQAR 254
 Qy 232 NTKISRPLKVLTIVVTFVTOLPNVIFCRADIIYSLTSNCNSKRMIAIQTESTI 291
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 255 NEERNKAIVKIVIAVVVFIVFOLPQNGVLAQTVANFNITSSCIELSKQNLNIAIDVTYSL 314
 Qy 292 ALFHSLNPLIVYFVGMASFKNYVMVKVAKKG-----SW-----RRQROSVEEFFD 337
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 315 ACVRCCVNPFMFLAFIGVKFRNDIFKLFKDLCGLSSEQLROWSCRHIRSSMSVE---- 359
 Qy 338 SGGTPTTS 349
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 370 ---AEHTTFS 377

RESULT 5
 JG5068
 G protein-coupled receptor CRK-L3 - human
 C Species: Homo sapiens (man)
 C Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C Accession: JG5068
 R Caballolos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A Title: Molecular cloning and RNA expression of two new human chemokine receptor-like q
 A Reference number: JG5067; MUID:97040707; PMID:8866020
 A Accession: JG5068
 A Molecule type: DNA
 A; Residues: 1-369 <ZAB>
 A; Cross-references: EMBL:279784; PIDN:g1668737; PIDN:CAB02144.1; PIDN:g1668738
 C; Comment: This protein belongs to the family of alpha chemoattractant receptors.
 A; Gene: GDB:CMKBR6; SIRL22; GPR39; CCR6; CRK-L3; GPR-CY4
 A; Cross-references: GDB:5370639; OMIM:601835
 A; Map position: 6q27-9q27
 C; Superfamily: vertebrate rhodopsin
 C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 C; Genetics:
 A; Cross-references: GDB:677463
 A; Note: Source clone K5-5
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1-360 <POW>
 A; Cross-references: GB:X85740; PIDN:g1370103; PIDN:CAA59743.1; PIDN:g971452
 A; Cross-references: GDB:CMKBR4
 A; Map position: 3p21-3p21
 C; Superfamily: vertebrate rhodopsin
 C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F; 40-65/Domain: transmembrane #status predicted <TM1>
 F; 40-65/Domain: transmembrane #status predicted <TM2>
 F; 40-65/Domain: transmembrane #status predicted <TM3>
 F; 76-97/Domain: transmembrane #status predicted <TM2>
 F; 112-133/Domain: transmembrane #status predicted <TM2>
 F; 151-175/Domain: transmembrane #status predicted <TM4>
 F; 203-226/Domain: transmembrane #status predicted <TM5>
 F; 291-308/Domain: transmembrane #status predicted <TM6>
 F; 243-264/Domain: transmembrane #status predicted <TM7>
 F; 29-276;110-187/Disulfide bonds: #status predicted
 F; 72,350/Binding site: phosphate (Ser) (covalent) (by kinase C) #status predicted
 F; 145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F; 183;194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F; 292-315/Domain: transmembrane #status predicted <TM7>
 Query Match 29 %; Score 537.5; DB 2; Length 360;
 Best Local Similarity 35.8%; Pred. No. 1.2e-38;
 Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;
 F; 115-136/Domain: transmembrane #status predicted <TM3>
 F; 160-180/Domain: transmembrane #status predicted <TM4>
 F; 212-233/Domain: transmembrane #status predicted <TM5>
 F; 250-271/Domain: transmembrane #status predicted <TM6>
 F; 292-315/Domain: transmembrane #status predicted <TM7>
 Query Match 32.1%; Score 533; DB 2; Length 369;
 Best Local Similarity 36.1%; Pred. No. 1.6e-42;
 Matches 121; Conservative 68; Mismatches 120; Indels 26; Gaps 7;

Query 8 STDYYEENMGTYDYSQYELICKDVERAKVFLPVFTIVFVGLAGSMVAYA 67
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 18 NTSTYSDSEM-----LICSLQEVROVSRFLPVFLAYSLICVGFGLNLVLTFA 67
 Qy 68 YKKORTKTDYIENLAVADLULIFTFLPWAV NAVHGWLGKIMCKITSALYTINVFVSG 126
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 68 FYKKARSKMDVYLMKARIDLFLVLTFLPWAVSHATGAWFMSATKLUKGJYALNCG 127
 127 MQFLACISIDRYVAVTKVPS---OSGYGKPCWMICFVWMAILISLIPOLFE--YTWN 179
 Qy 128 MLLJACISMDRFLYIAVQATSKSFLRSRTLPRSKTICLVWVGJWSVISSSTFFNOKINTQ 187
 Qy 180 DNARCIPPFYKLGTSKALIQMLEICIGFVPPFLIMGVCFYFPARTLKMKPNIKSP 238
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 183 LACISTDRYVAVTKV-----PSOSGVGPWCWITCFCWWMAILLSIOLVF--YTWN 179
 Qy 130 KORTKTDYIENLAVADLULIFTFLPWAV NAVHGWLGKIMCKITSALYTINVFVSG 129
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 128 VMLMSIDRYIAYAVHAFSLRARTLTYGV---ITSLAWWSVAVASLGFGLFCYTER 182
 Qy 180 DNARCIPPFYKLGTSKALIQMLEICIGFVPPFLIMGVCFYFPARTLKMKPNIKSP 238
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 183 NHYTKKYS---LNSTWKVLSLENLIGVLPVGFIMFCYSMIRITQHCKNEKNA 240
 239 LKVLTWVINVTFOLPYIVKFCRADIIYSLTSNCNSKRMIAIQTESTIAFLHSCL 298
 Qy 241 VRMFIAVWFLFGLFWPYVFLFLEL-VELEVQDCTPERYDIAQTETLAFVHCCL 299
 Qy 299 NPFLYVFMASFKNYVMVK 319

A;Experimental source: peripheral blood mononuclear cell
 C;Comment: This protein is a cell-surface receptor which recognizes extracellular signal
 C;Comment: This protein is a key regulator of many immune and homeostatic responses, and
 C;Genetics:
 A;Gene: v28
 A;Map position: 3pter-p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; Lymphokine; transmembrane protein
 F;35-57;/Domain: transmembrane #status predicted <TM1>
 F;66-88;/Domain: transmembrane #status predicted <TM2>
 F;104-125;/Domain: transmembrane #status predicted <TM3>
 F;146-165;/Domain: transmembrane #status predicted <TM4>
 F;197-217;/Domain: transmembrane #status predicted <TM5>
 F;230-254;/Domain: transmembrane #status predicted <TM6>
 F;275-295;/Domain: transmembrane #status predicted <TM7>
 Query Match 28.7%; Score 522.5; DB 2; Length 355;
 Best Local Similarity 36.4%; Pred. No. 2.4e-37;
 Matches 112; Conservative 57; Mismatches 122; Indels 17; Gaps 5;
 Matches 112; Conservative 57; Mismatches 122; Indels 17; Gaps 5;
 Qy 22 YDYSQVELICKEIDVREBFAKVFLPVLITIVFVIGLAGNSMVATAYYKQRTKDVIIL 81
 Db 12 FEYDDLAECYIGDINVFGTVPLSIVSYVFAIGLYGNLNVFALTNSKKSVRDIVYL 71
 Qy 82 NEAVADILLLFLPFNAWNAHGWGWLKGKMKRITSALTYLTNUFSGKQFLACISIDRYVYU 141
 Db 72 NLASLDLIFLAVTLPFWTHYLNEKGHLNAMCKTATTFFIGFGSISFFITVISIDRLYL 131
 Qy 142 TKVPS-----OSGVQKPCWICFCVWWMAILSILSPQLVYFTVNNDNARCIPIFPRYLT 194
 Db 1312 VLAANSNNRNYQHGV----TISLGWVAATLVAAPOFMPTKQEN-ECLGDPYPEVQE 185
 Qy 195 SMKALIONLEICIGFVVFFPLMGVCYITARTILMKMPNIKSRLPKVLTWIVFIVQL 254
 Db 186 IMPVLRNWTNFQFLPLIMSYCERLIQTLFSCKRNKAIAKILVWIVFELWT 245
 Qy 255 PYNNVKCRAIDIYLSITSTCSNNKRMIDATQTESTALFHGCCLNPILYVNGASFRNN 314
 Db 246 PYNMIFLETKL-LYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYFAGEKFRRYL 304
 Qy 315 MKVAKKG 322
 Db 305 YHL---YG 309

RESULT 10

JC4587 chemokine (C-C) receptor 4 - mouse
 C;Species: *Mus musculus* (house mouse)
 C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 C;Accession: JC4587
 Biochemical: Biophys. Res. Commun. 218, 337-343, 1996
 A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A;Reference number: JC4587; MUID:96136324; PMID:8573157
 A;Accession: JC4587
 A;Molecule type: mRNA
 A;Cross-references: EMBL:x90862; NID:91167851; PID:CAA62372.1; PID:91167852
 A;Experimental sources: thymus
 A;Experiments:
 A;Genes:
 A;Gene: cc ckr-4
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F;2-183-194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;72-202-350/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;231/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 Query Match 28.7%; Score 522.5; DB 2; Length 360;
 Best Local Similarity 33.7%; Pred. No. 2.4e-37;
 Matches 110; Conservative 69; Mismatches 128; Indels 19; Gaps 6;

Db 303 AFLGLPFRQDRLRLRGSSPGQPQRGCPRRPLS-----SCSAPTEHSL 350
 RESULT 12
 A53752
 Interleukin-8 receptor (clone 5B1a) - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C;Accession: A53752
 R;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J.; Biol. Chem. 269, 12391-12394, 1994
 A;Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
 A;Reference number: A53752; MUID:94230294; PMID:8175642
 A;Cross-references: GB:<PRA>
 A;Molecule type: mRNA
 A;Residues: 1-358 <PRA>
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein
 C;Keywords: G protein-coupled receptor; transmembrane protein
 Query Match 27.6%; Score 501.5; DB 2; Length 355;
 Best Local Similarity 33.1%; Pred. No. 1.5e-35;
 Matches 107; Conservative 70; Mismatches 127; Indexes 19; Gaps 6;
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Cross-references: GB:<PRA>
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein
 Query Match 28.1%; Score 511; DB 2; Length 358;
 Best Local Similarity 32.3%; Pred. No. 2.3e-36;
 Matches 116; Conservative 72; Mismatches 139; Indexes 32; Gaps 8;
 QY 10 DYYVNEENEMGTDYSQVELI-----CIKEKDVREFAKVLPVELTIVFVIGLA 57
 8 NYSE-E-DFFG-DFSNSVSYSTDLPTILDSACRCSLESLETSNYYVLLITY-LVFLSSL 62
 QY 58 GNSAWAVATAYKKORTKDVTYLNLAVALDILLFETPFWANAVAHWVLGKIMCKITSA 117
 Db 63 GNSLVMVLYLISYSSTCSVTDVILNLADLFTLPIWAASKVHGWTFGTPLKVKWL 122
 QY 118 LYTFNFVSGMQLFACISDRYVA---TKPSQSGVKPCWICFCVWMAAIIISIPL 172
 Db 123 VKEVNFKYSGILLACISVDRYLAVIAHTRTMQKHLVY---FICLSMMQVSILSPL 178
 QY 173 LVIYVNDNARCIPIPPRLGTS--MKALIQMLEICIGFWVPPFLTMGVCFITARTPLMK 229
 Db 179 LILRNATIAPPNNSPPVCYEDMGNSTAKRMVLRLPQFGFLPLPFLYMLFCVFTLTLFQ 238
 QY 230 MPWKISRPLKVLLTVVIFVIFOLPYNIKFCRAIDIYSLTSNCNSKRMIDAIQVTESELFSCLN 289
 Db 239 AHNGQKHARMVYFAVFLFLICWLPNVLVLTDLMRTHVIOETCERRNDIDRALDATE 298
 QY 290 SIALFHSLNPILYVFMGASFKNYVMVAKKYGWSRQ---RQSYEEFPDSEGTEPT 345
 Db 299 ILGFLHSCLNPITIYAFIGOKEYGLKILAAHGLISKEFLAKERSPSFVAASSGNST 357
 RESULT 13
 JO1231
 Interleukin-8 receptor - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
 C;Accession: JO1231; A46483
 R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard, J.; Immunol. 179, 784-789, 1991
 A;Title: Molecular characterization of the interleukin-8 receptor.
 A;Reference number: JO1231; MUID:91378994; PMID:1898400
 A;Accession: JO1231
 A;Molecule type: DNA
 A;Residues: 1-355 <BCR>
 A;Cross-references: GB:M74240; NID:9165438; PIDN:AAA31375.1; PID:9165439
 R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
 J.; Immunol. 148, 1261-1264, 1992
 A;Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
 A;Reference number: A46483; MUID:92148149; PMID:1737938
 A;Accession: A46483
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-355 <PFE>
 A;Cross-references: GB:<PFE>
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-352 <PFE>
 A;Cross-references: EMBL:X71635; NID:9290099; PIDN:CAA50641.1; PID:9297100
 R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
 DNA Cell Biol. 12, 465-471, 1993
 A;Title: Molecular cloning, characterization, and localization of the human homolog t
 A;Reference number: I53103; MUID:93319629; PMID:8276799
 A;Accession: A53103
 A;Molecule type: mRNA
 A;Residues: 1-352 <LOE>
 A;Cross-references: EMBL:X71635; NID:9290099; PIDN:CAA50641.1; PID:9297100
 R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
 DNA Cell Biol. 12, 465-471, 1993
 A;Title: Molecular cloning, characterization, and localization of the human homolog t
 A;Reference number: I53103; MUID:93319629; PMID:8276799
 A;Accession: I53103
 A;Molecule type: mRNA
 A;Residues: 1-352 <HER>
 A;Cross-references: GB:L06797; NID:9414929; PIDN:AAA03209.1; PID:9414928
 R;Engel, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Meng, G.; Walker, M.W.; Salom, J.; Regul. Pept. 47, 247-258, 1993
 A;Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolog.
 A;Reference number: I59444; MUID:94052833; PMID:8234909
 A;Accession: I59444
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Cross-references: GB:M92873; NID:9165440; PIDN:AAA31376.1; PID:9165441
 A;Molecule type: mRNA
 A;Cross-references: GB/EMBL/DDJB

A; Residues: 1-352 <RE2>
 A; Cross-references: GB:L01639; NID:9189313; PIDN:AAA16594.1; PID:9189314
 R; Nomura, H.; Nielsen, B.W.; Matsushima, K.
 Int. Immunol., 5, 1239-1249, 1993
 A; Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotaxis receptor number: 154751; MUID:94092629; PMID:7505609
 A; Accession: 169203
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: mRNA
 A; Residues: 1-352 <RES>
 A; Cross-references: GB:D10924; NID:9219868; PIDN:BAAQ1722.1; PID:9219869
 C; Genetics:
 A; Gene: GDB:NPY3R; NPYY3
 A; Cross-references: GDB:230002; OMIM:162643
 A; Map position: 2q21-2q21
 C; Superfamily: vertebrate rhodopsin
 C; Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.5%; Score 500.5; DB 2; Length 352;
 Best Local Similarity 34.6%; Pred. No. 1.8e-35; Gaps 4;
 Matches 107; Conservative 57; Mismatches 134; Indels 11; Gaps 4;

Db 71 RSMTDKYRLHSVADLFLFVLTLPFWAVADAVANWTFEGKELGKAVHIVYTVDYSSVLILAF 130
 Qy 133 ISIDRVAVTKVPSQSVCVGPCT---WTCFCVWWMAILSISIOLPV--YTWNDRAC 184
 Db 131 ISLDYLAIVATNSO--KCRKLAEKVYVVGMLPAVILTPDIFAKEDIVEYRC 187
 Qy 185 IPIFPRVLTGSMKALIOMLEICIGFVVPFLIMGCVYFITARTLMMKMPNPKISRPKVLLT 244
 Db 188 DRFVPSDL--WLWVQFOHQHIVGLLPGIVLSCYCIIASKLSKGQKRKAHTVY 244
 Qy 245 VVIVFTVOLPYNIVFCRAADITYSLITSNCNSKMDIAQVTESIALHSCLNPILY 304
 Db 245 LITFFACWMLPYIGISIDSFILEI1QOCCEPESTIVHKWISITEBALAFFHCCLNPILY 304
 Qy 305 FNGASEFK 311
 Db 305 FIGAKFK 311

Search completed: March 14, 2003, 16:12:36
 Job time : 20 secs

RESULT 15
 S28787

neuropeptide Y peptide YY receptor Y3 - bovine
 C; Species: Bos primigenius taurus (cattle)

C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999

C; Accession: S28787

R; Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.

MOL Pharmacol. 40, 869-875, 1991

A; Title: Sequence and expression of a neuropeptide Y receptor cDNA.

A; Reference number: S28787; MUID:92100053; PMID:1661837

A; Accession: S28787

A; Molecule type: mRNA

A; Residues: 1-353 <RES>

A; Cross-references: EMBL:M86739

C; Superfamily: vertebrate rhodopsin

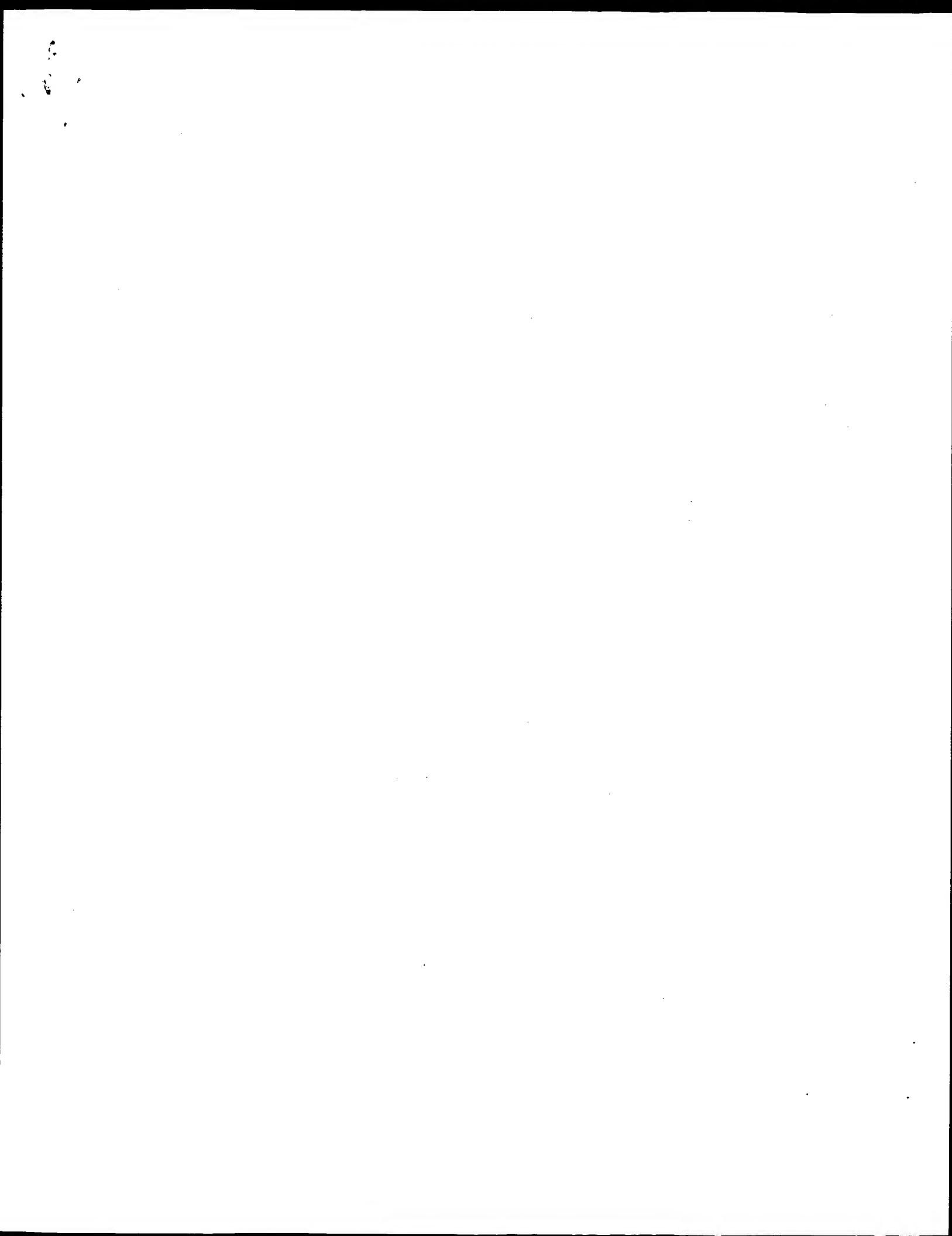
C; Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 27.5%; Score 499.5; DB 2; Length 353;

Best Local Similarity 34.5%; Pred. No. 2.2e-35; Gaps 5;

Matches 106; Conservative 60; Mismatches 126; Indels 15; Gaps 5;

Qy 13 YEEENEANGTVTDYSQYELICIDKEFAVKFLPFLTVFVLAGNSVVAIAYVKKQ 72
 Db 12 YTEDDL-GSGDYDSMKEPCFRENAHFRIFLPVSYIIFLTGIVGNGLVLYGMQKKL 70
 Qy 73 RKTDVYLNLAVADLILFLPFWAVNAVHGWLKGKIMKITASLYTINFVSQMFAC 132



PT modulating inflammation and tumor growth
 XX
 PS Claim 8; Fig 2A-B; 123pp; English.
 XX
 CC The invention relates to a human BGCKr protein, a G-protein coupled receptor. The BGCKr protein can be expressed by standard recombinant methodology. BGCKr are receptor proteins possibly involved in modulation of proinflammatory or stimulatory functions of chemokines, cell proliferation, migration, adhesion and targeting, and exocytosis. The CC nucleic acids and derived proteins (or their variants), antibodies and modulators are potentially useful for modulating inflammation, tumour growth, allergic reactions and entry of human immune deficiency virus into cells, for therapeutic or prophylactic purposes. They are also CC used for diagnosis and in drug-screening assays. The present sequence represents the full-length human BGCKr protein.

SQ sequence 350 AA;

Query Match 100.0%; Score 1819; DB 20; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.9e-195; Mismatches 0; Indels 0; Gaps 0;
 Matches 350; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 MALEONQSTDYVYENEMGTVDSQYELICKEDREFAKVFLPVLTIVFVLAGNS 60
 Db 1 MALEONQSTDYVYENEMGTVDSQYELICKEDREFAKVFLPVLTIVFVLAGNS 60
 QY 61 MWAIAYAYKKORTKTDVYLNLAVADLLTLPFWAVAVWAVHVGKIMCMTSALYT 120
 Db 61 MWAIAYAYKKORTKTDVYLNLAVADLLTLPFWAVAVWAVHVGKIMCMTSALYT 120
 QY 121 LNFVSGMOLFACISIDRYVATKVPSQSGVKGPCWICFCVWMAAILLSIOLVFTVND 180
 Db 121 LNFVSGMOLFACISIDRYVATKVPSQSGVKGPCWICFCVWMAAILLSIOLVFTVND 180
 QY 181 NARCIPIFPRYGTSMKALIQMLECTIGFVPRFLMGCVYFTARTLKMKNIKSRPLK 240
 Db 181 NARCIPIFPRYGTSMKALIQMLECTIGFVPRFLMGCVYFTARTLKMKNIKSRPLK 240
 QY 301 ILYVFMGASKNYMKVAKKGWRQRQSVEEFPDSEGPTEPISTSI 350
 Db 301 ILYVFMGASKNYMKVAKKGWRQRQSVEEFPDSEGPTEPISTSI 350
 RESULT 2
 AAY17435
 ID AAY17435 standard; Protein; 350 AA.
 XX
 AC AAY17435;
 XX
 DT 29-JUL-1999 (first entry)
 DE Human signal peptide-containing protein SP-16.
 XX
 KW Human; signal peptide-containing protein; SP; cell proliferation; cancer; neuronal disorder; immune response; detection.
 OS Homo sapiens.
 PN W0924463-A2.
 XX
 PD 20-MAY-1999.
 XX
 PP 04-NOV-1998; 98WO-US23578.
 PR 07-NOV-1997; 97US-0966316.
 PA (INCY-) INCYTE PHARM INC.
 XX
 PN

PI Au-Young J, Lal P, Mathur P, Murry LE, Ready R;
 XX DR WPI; 1999-337694/28.
 XX N-PSDB; AAX61388.
 PT cDNA clones encoding signal peptide-containing proteins
 XX
 PS Claim 1; Fig 1; 83pp; English.
 XX
 CC The present sequence represents a human signal peptide-containing protein (SP), designated SP-16. SP proteins can be used to stimulate cell proliferation or to treat or prevent cancer. SP antagonists are also used to treat or prevent cancer, and also for treating or preventing neuronal disorders or immune responses. Polynucleotide sequences complementary to the SP-encoding nucleic acid molecules are useful for the detection of SP-encoding nucleic acid molecules in biological samples.

SQ sequence 350 AA;

Query Match 100.0%; Score 1819; DB 20; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.9e-195; Mismatches 0; Indels 0; Gaps 0;
 Matches 350; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 MALEONQSTDYVYENEMGTVDSQYELICKEDREFAKVFLPVLTIVFVLAGNS 60
 Db 1 MALEONQSTDYVYENEMGTVDSQYELICKEDREFAKVFLPVLTIVFVLAGNS 60
 QY 61 MWAIAYAYKKORTKTDVYLNLAVADLLTLPFWAVAVWAVHVGKIMCMTSALYT 120
 Db 61 MWAIAYAYKKORTKTDVYLNLAVADLLTLPFWAVAVWAVHVGKIMCMTSALYT 120
 QY 121 LNFVSGMOLFACISIDRYVATKVPSQSGVKGPCWICFCVWMAAILLSIOLVFTVND 180
 Db 121 LNFVSGMOLFACISIDRYVATKVPSQSGVKGPCWICFCVWMAAILLSIOLVFTVND 180
 QY 181 NARCIPIFPRYGTSMKALIQMLECTIGFVPRFLMGCVYFTARTLKMKNIKSRPLK 240
 Db 181 NARCIPIFPRYGTSMKALIQMLECTIGFVPRFLMGCVYFTARTLKMKNIKSRPLK 240
 QY 301 ILYVFMGASKNYMKVAKKGWRQRQSVEEFPDSEGPTEPISTSI 350
 Db 301 ILYVFMGASKNYMKVAKKGWRQRQSVEEFPDSEGPTEPISTSI 350
 RESULT 3
 AAW93169
 ID AAW93169 standard; Protein; 350 AA.
 XX
 AC AAW93169;
 XX
 DT 24-MAY-1999 (first entry)
 DE Human HFTA041 protein.
 XX
 KW HFTA041; G-coupled receptor; disease susceptibility; diagnosis; immunise; inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer; diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; allergy; angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia; benign prostatic hypertrophy; psychotic disorder; neurologic disorder; anxiety; manic depression; delirium; dementia; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; linkage analysis; gene mapping; human.
 OS Homo sapiens.
 XX
 PN EP899332-A2.

Sequence 350 AA; accession vector for production of receptor polypeptides in host cells. The polypeptides can be used to identify agent which modulate VSHR-1 receptor signal transduction

QY 301 ILYVFMGASFKNYVMVAKKYGSSWRQROROSVEEFPFDSEGTEPEPTSTFSI 350
 Db ID AAB62389 standard; Protein; 382 AA.
 Db 301 ILYVFMGASFKNYVMVAKKYGSSWRQROROSVEEFPFDSEGTEPEPTSTFSI 350

RESULT 8
 AAB62389
 ID AAB62389 standard; Protein; 382 AA.
 XX
 AC AAB62389;
 XX
 DT 29-JUN-2001 (first entry)
 XX
 DE Human chemokine receptor CCX CKR polypeptide.
 XX
 Chemokine receptor; CCX CKR; chemokine; ELC; SLC; TECCK; modulator; antiinflammatory; immunosuppressive; cytostatic; antiallergic; human; KW immunosuppressant; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 351
 FT /note= "encoded by TAA"
 FT Misc-difference 353
 FT /note= "encoded by TAA"
 FT Misc-difference 365
 FT /note= "encoded by TGA"
 FT Misc-difference 371
 FT /note= "encoded by TAA"
 XX
 PN WO200127146-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 10-OCT-2000; 2000WO-US28067.
 XX
 PR 12-OCT-1999; 99US-0159015.
 PR 13-OCT-1999; 99US-0159210.
 PR 20-DEC-1999; 99US-0172979.
 PR 28-DEC-1999; 99US-0173389.
 PR 03-MAR-2000; 2000US-0186626.
 XX
 PA (CHEM-) CHEMOCENTRUM INC.
 XX
 PT Gosling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;
 XX
 DR N-PSDB; AAF57685.
 XX
 PT Isolated or recombinant chemokine receptor (designated CCX CKR) polypeptide (P1) or its fragment, useful for identifying CCX CKR modulators which can be used in the treatment of inflammation, allergy, an autoimmune disease or cancer -
 XX
 PS Claim 4; Fig 1; 72pp; English.
 XX
 CC The invention relates to an isolated or recombinant chemokine receptor (designated CCX CKR) polypeptide which binds to chemokines such as ELC, SLC or TECCK. The CCX CKR polypeptide is useful for identifying CCX CKR modulators. An agent that modulates the activity or expression of CCX CKR in a cell or tissue in the mammal is useful in the treatment of a CCX CKR -mediated condition such as inflammation, allergy, an autoimmune disease, graft rejection, cancer, an infectious disease or an immunosuppressive disease. The present sequence represents the human CCX CKR polypeptide.
 XX
 SQ Sequence 382 AA;

Query Match 100.0%; Score 1819; DB 22; Length 382;
 Best Local Similarity 100.0%; Pred. No. 2; 2e-195; Mismatches 350; Conservative 0; Indels 0; Gaps 0;

QY 1 MALEONQSTDYYEENENGTYDYSQELICITKEDREFARKVFLPVFLTIVVIGLAGNS 60
 Db ID 1 MALBONOSTDYYEENENGTYDYSQELICITKEDREFARKVFLPVFLTIVVIGLAGNS 60
 Db 61 MVAVAYAKKQRTKDVLNLAVADLLFLPFWAVNVAVHGWLGKIMCKITSALI 120
 QY 181 NARCIPIFPRYLGSKMAJLQMCIFICIGRVVPLIMGCVYETARTLMKMPNIKSRPLK 240
 Db ID 181 NARCIPIFPRYLGSKMAJLQMCIFICIGRVVPLIMGCVYETARTLMKMPNIKSRPLK 240
 QY 241 VLTIVVIVFTQLPNIVKFCRAIDIYSLTSNCNSKRMQIAQTESTALFHSLNP 300
 Db ID 241 VLTIVVIVFTQLPNIVKFCRAIDIYSLTSNCNSKRMQIAQTESTALFHSLNP 300
 QY 301 ILYVFMGASFKNYVMVAKKYGSSWRQROROSVEEFPFDSEGTEPEPTSTFSI 350
 Db ID 301 ILYVFMGASFKNYVMVAKKYGSSWRQROROSVEEFPFDSEGTEPEPTSTFSI 350

RESULT 9
 RAW93170
 ID AAW93170 standard; Protein; 349 AA.
 XX
 AC AAW93170;
 XX
 DT 24-MAY-1999 (first entry)
 XX
 DE Human HFTAO41 protein.
 XX
 HFTAO41; G-coupled receptor; disease susceptibility; diagnosis; immunise; treatment; FTAO41 protein; gene therapy; immune response; vaccine; HIV-2; inoculate; bacterial; fungal; protozoan; virus; infection; HIV-1; cancer; KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure; KW hypotension; hypertension; urinary retention; osteoporosis; allergy; KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia; KW benign prostatic hypertrophy; psychotic disorder; neurological disorder; KW anxiety; manic depression; delirium; dementia; severe mental retardation; KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; KW linkage analysis; gene mapping; human; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP899332-R.
 XX
 PD 03-MAR-1999.
 XX
 PF 17-FEB-1998; 98EP-0301170.
 XX
 PR 27-OCT-1997; 97US-0962922.
 PR 15-AUG-1997; 97US-0055895.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Ellis CE;
 XX
 DR WPI; 1999-144803/13.
 DR N-PSDB; AAX22558.

XX
 Disclosure; Page 25-26; 27pp; English.

XX
 CC This sequence encodes a G-coupled receptor, HFTAO41 which is useful for diagnosing susceptibility to diseases by detecting mutations in the HFTAO41 gene, and can diagnose diseases associated with HFTAO41 protein imbalance by determining HFTAO41 polypeptide expression levels. Monists

and antagonists of the protein can be used in treatment to activate (agonist) or inhibit (antagonist) HFTA041 activity, in addition to direct administration of antisense sequences to prevent expression, or HFTA041 polynucleotides to treat conditions associated with a lack of HFTA041 protein. Gene therapy may also be used to affect endogenous HFTA041 polypeptide expression. HFTA041 antibodies are useful for inducing an immune response to immunise and prevent disease, and for isolating HFTA041 clones or purifying the polypeptides by affinity chromatography. HFTA041 polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, prevented and treated include bacterial, fungal, protozoan and viral infections, particularly HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcers; asthma; allergies; benign prostatic hypertrophy; and psychiatric and neurological disorders, including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease or Gilles de la Tourette's syndrome. The HFTA041 polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis.

XX Sequence 349 AA;

Query Match 99.7%; Score 1814; DB 20; Length 349; Best Local Similarity 100.0%; Pred. No. 7e-195; Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALERONQSTDYYEEENEMGTYDSOYELICKEIDVREFAKVFLPVFLTVFVIGLAGNS 61
Db 1 ALERONQSTDYYEEENEMGTYDSOYELICKEIDVREFAKVFLPVFLTVFVIGAGNS 60
QY 62 VVAVIAYYKQRTKTDVYILNLAVALLFLTPFWAVNAVHGWLGKIMCKITSALYT 121
61 VVAVIAYYKQRTKTDVYILNLAVALLFLTPFWAVNAVHGWLGKIMCKITSALYT 120
QY 122 NEVSGMQLACISIDRYVAVTKVPSQSGVKGPCWICFCWVMMAILSIPOLVFVYNDN 181
Db 121 NEVSGMQLACISIDRYVAVTKVPSQSGVKGPCWICFCWVMMAILSIPOLVFVYNDN 180
QY 182 ARCPICIPPRYLTGTSMKALIQMLEICIGFWVFLMGVCYFTARTLMKMPNIKSRLKV 241
Db 181 ARCPICIPPRYLTGTSMKALIQMLEICIGFWVFLMGVCYFTARTLMKMPNIKSRLKV 240
QY 242 LLTVWIVFVFLQPYNTVKFCRAIDIYSLITSCNMKRMEDIAQTESTIALFHCLNP 301
Db 241 LLTVWIVFVFLQPYNTVKFCRAIDIYSLITSCNMKRMEDIAQTESTIALFHCLNP 300
QY 302 LYVFMGASFKNYVAKKYGSRRQRQSVEEFPDSEGPTEPPTFSI 350
Db 301 LYVFMGASFKNYVAKKYGSRRQRQSVEEFPDSEGPTEPPTFSI 349

PR 24-DEC-1997; 97JP-0354537.
XX XX
CC PA (ASAHI KASEI KOGYO KK.
CC XX
CC PT Ishinaru H, Koshio T, Ohno T;
CC DR WPI: 1999-493806/41.
CC DR N-PSB; AAX86674.
XX PT New seven-pass transmembrane receptor protein useful for treating,
CC preventing or diagnosing autoimmune diseases
CC XX
CC The present sequence represents a seven-pass transmembrane receptor protein. The protein and its DNA can be used to screen substances for the diagnosis, prevention and treatment of autoimmune diseases, particularly those due to white blood cell dysfunction.
CC XX
CC Sequence 350 AA;
Query Match 99.7%; Score 1814; DB 20; Length 350; Best Local Similarity 99.7%; Pred. No. 7e-195; Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Gaps 0;
QY 1 MALEONQSTDYYEEENEMGTYDSOYELICKEIDVREFAKVFLPVFLTVFVIGAGNS 60
Db 1 MALBONQSTDYYEEENEMGTYDSOYELICKEIDVREFAKVFLPVFLTVFVIGAGNS 60
QY 61 MVAVIAYYKQRTKTDVYILNLAVALLFLTPFWAVNAVHGWLGKIMCKITSALYT 120
Db 61 MVAVIAYYKQRTKTDVYILNLAVALLFLTPFWAVNAVHGWLGKIMCKITSALYT 120
QY 121 LNFGSGMQLACISIDRYVAVTKVPSQSGVKGPCWICFCWVMMAILSIPOLVFVYND 180
Db 121 LNFGSGMQLACISIDRYVAVTKVPSQSGVKGPCWICFCWVMMAILSIPOLVFVYND 180
QY 181 NARCPIPPRYLTGTSMKALIQMLEICIGFWVFLMGVCYFTARTLMKMPNIKSRLKV 240
Db 181 NARCPIPPRYLTGTSMKALIQMLEICIGFWVFLMGVCYFTARTLMKMPNIKSRLKV 240
QY 241 VLLTVWIVFVFLQPYNTVKFCRAIDIYSLITSCNMKRMEDIAQTESTIALFHCLNP 300
Db 241 VLLTVWIVFVFLQPYNTVKFCRAIDIYSLITSCNMKRMEDIAQTESTIALFHCLNP 300
QY 301 LYVFMGASFKNYVAKKYGSRRQRQSVEEFPDSEGPTEPPTFSI 350
Db 301 LYVFMGASFKNYVAKKYGSRRQRQSVEEFPDSEGPTEPPTFSI 350

RESULT 11

AAV71301 ID AAV71301 standard; Protein: 350 AA.

XX ID AAV71301; AC AAV71301;
XX AC AAV71301;
XX DT 02-NOV-2000 (first entry)DE Human orphan G protein-coupled receptor hpprl.
XX Human; orphan G protein-coupled receptor; GPCR; hpprl; drug screening;
KW transmembrane receptor; expressed sequence tag; EST; signal cascade.
XX OS Homo sapiens.
XX PN WO20031258-A2.
PN PD 02-JUN-2000.
XX PR 13-OCT-1999; 99WO-US23687.
XX PR 20-NOV-1998; 98US-0109213.
PR 16-FEB-1999; 99US-0120416.

RESULT 10

AAV30125 ID AAV30125 standard; Protein: 350 AA.

XX AC AAV30125;
XX DT 14-OCT-1999 (first entry)

DE A human seven-pass transmembrane receptor protein.
XX Seven-pass transmembrane receptor; autoimmune disease;
KW white blood cell dysfunction.

XX OS Homo sapiens.

XX PN WO9933876-A1.
XX PD 08-JUL-1999.
XX PR 24-DEC-1998; 98WO-JP05886.

PR	26-FEB-1999;	99US-0121852.	Db	241	
PR	12-MAR-1999;	99US-0123946.	VLLTVVIVFVTQLPNYYKFCRAIDIYSLITSCNMRSKRMIDAIQVTESTALFHSCLN		
PR	12-MAR-1999;	99US-0123949.	300		
PR	28-MAY-1999;	99US-0136435.	QY		
PR	28-MAY-1999;	99US-0136437.	ILYVPGASKNYVKVAKKGYSRRQRROSSEERPDSEGPTPEPTFSI		
PR	28-MAY-1999;	99US-0136439.	350		
PR	28-MAY-1999;	99US-0137127.	Db		
PR	28-MAY-1999;	99US-0137131.	301		
PR	29-JUN-1999;	99US-0141448.	ILYVPGASKNYVKVAKKGYSRRQRROSSEERPDSEGPTPEPTFSI		
PR	29-SEP-1999;	99US-0156633.	350		
PR	29-SEP-1999;	99US-0156634.	AC		
PR	29-SEP-1999;	99US-0156653.	AAB02835;		
PR	01-OCT-1999;	99US-0157280.	XX		
PR	01-OCT-1999;	99US-0157281.	DT		
PR	01-OCT-1999;	99US-0157282.	XX		
PR	01-OCT-1999;	99US-0157293.	DE		
PR	01-OCT-1999;	99US-0157294.	Human G protein coupled receptor hPPR1 protein SEQ ID NO:24.		
PR	01-OCT-1999;	99US-0416760.	KW		
PR	12-OCT-1999;	99US-0417044.	Human; G protein coupled receptor; GPCR; transmembrane receptor; identification; agonist; screening; therapeutic; pharmaceutical; mutant.		
PA	(AREN-) ARENA PHARM INC.	XX	KW		
PA	Chen R, Dang HT, Liaw CW, Lin T;	OS	XX		
PI	XX	Homo sapiens.	XX		
DR	XX	PN	XX		
DR	N-PSDB; AAD01128.	WO20022131-A2.	XX		
PT	Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists -	XX	XX		
PT	Claim 42; Page 69-70; 102pp; English.	PD	XX		
PS	CC	PF	XX		
The present amino acid sequence is the hPPR1, an endogenous human orphan G protein-coupled receptor (GPCR), expressed in the pituitary gland, heart, salivary gland, small intestine and testis. The hPPR1 cDNA was identified using EST (expressed sequence tag) AA359304 and 238667 as a probe. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in healthy and pathological states.	13-OCT-1999;	99WO-US24065.	PR		
CC	CC	PR	13-OCT-1998;	99US-0174946.	PR
CC	CC	PR	12-NOV-1998;	99US-019213.	PR
CC	CC	PR	20-NOV-1998;	99US-019213.	PR
CC	CC	PR	27-NOV-1998;	99US-010060.	PR
CC	CC	PR	16-FEB-1999;	99US-0120416.	PR
CC	CC	PR	26-FEB-1999;	99US-0121852.	PR
CC	CC	PR	12-MAR-1999;	99US-0123944.	PR
CC	CC	PR	12-MAR-1999;	99US-0123945.	PR
CC	CC	PR	12-MAR-1999;	99US-0123946.	PR
CC	CC	PR	12-MAR-1999;	99US-0123947.	PR
CC	CC	PR	12-MAR-1999;	99US-0123948.	PR
CC	CC	PR	12-MAR-1999;	99US-0123949.	PR
CC	CC	PR	12-MAR-1999;	99US-0123951.	PR
CC	CC	PR	28-MAY-1999;	99US-0134336.	PR
CC	CC	PR	28-MAY-1999;	99US-0134337.	PR
CC	CC	PR	28-MAY-1999;	99US-0134339.	PR
CC	CC	PR	28-MAY-1999;	99US-0137127.	PR
CC	CC	PR	28-MAY-1999;	99US-0137131.	PR
CC	CC	PR	28-MAY-1999;	99US-0137282.	PR
CC	CC	PR	30-JUN-1999;	99US-0141448.	PR
CC	CC	PR	27-AUG-1999;	99US-0151114.	PR
CC	CC	PR	03-SEP-1999;	99US-0152524.	PR
CC	CC	PR	29-SEP-1999;	99US-0156633.	PR
CC	CC	PR	29-SEP-1999;	99US-0156634.	PR
CC	CC	PA	(AREN-) ARENA PHARM INC.	XX	PA
QY	1 MALEQONQSTDYVYEEENGTGTYDYSQVELICKEDREFAKVFLPVFLTVFVIGLAGNS 60	XX	Behan DP, Leinmann-Bruinsma K, Chalmers DR, Chen R, Dang HT;	XX	PT
Db	1 MALEQONQSTDYVYEEENGTGTYDYSQVELICKEDREFAKVFLPVFLTVFVIGLAGNS 60	XX	Gore M, Liaw CW, Lin T, Lowitz K, White C;	XX	PT
Oy	61 MVVAVIAYVKKRDKTQVTLINAVADLILETPFWAVNAVHGWLGKIMCKITSALY 120	XX	DR	WPI; 2000-317986/27.	WPI
Db	61 MVVAVIAYVKKRDKTQVTLINAVADLILETPFWAVNAVHGWLGKIMCKITSALY 120	XX	DR	N-PSDB; AAC46029.	WPI
Oy	121 LNFVSGMQLFLACTISDRYAVAVTRVPSQSGVGKPCWLTCFCVWMAATLISPOLVFTVND 180	XX	PT	Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents -	PT
Db	121 LNFVSGMQLFLACTISDRYAVAVTRVPSQSGVGKPCWLTCFCVWMAATLISPOLVFTVND 180	XX	PT	Example 1; Page 99-100; 187pp; English.	PT
Qy	181 NACIPIFPRYLGTSMLAQMELICIGFVWPLFLMCYFTRATLKMNPNIKSRPLK 240	XX	CC	The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCRs), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for	CC
Db	181 NACIPIFPRYLGTSMLAQMELICIGFVWPLFLMCYFTRATLKMNPNIKSRPLK 240	XX	CC	CC	CC
Qy	181 NACIPIFPRYLGTSMLAQMELICIGFVWPLFLMCYFTRATLKMNPNIKSRPLK 240	XX	CC	CC	CC
Qy	241 VLTWVIVFIVIQDLPNIVKFRRAIDIYSLITSCMSKRDIAIOTVESIRALHSCLNP 300	XX	CC	CC	CC

CC the direct identification of candidate compounds as receptors agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAA40117 to AAA46126 and AAB2825 to AAB2859 represent sequences used in
 CC the exemplification of the present invention.

XX SQ Sequence 350 AA;

Query Match 99.5%; Score 1810; DB 21; Length 350;
 Best Local Similarity 99.4%; Pred. No. 2e-194; Matches 348; Conservative 0; Indels 0; Gaps 0;
 Mismatches 2; Associated with the disorder in a G-protein mediated pathway. They are
 QY 1 MALEQNOSTDYVYENEMGTYDYSQELYCICKEDVREFAKVFLPVFLTVFVIGLAGNS 60
 1 MALEQNOSTDYVYENEMGTYDYSQELYCICKEDVREFAKVFLPVFLTVFVIGLAGNS 60

Db 61 MVAIAYKKORTKTDVYLNLAVADLLFLPFWAVNAVHGVWLGKIMCKTSALYT 120
 61 MVAIAYKKORTKTDVYLNLAVADLLFLPFWAVNAVHGVWLGKIMCKTSALYT 120

Db 121 LNFMGASFKNYVMVKYKGSRQRQSVEEFPDSEGPTEPTSTSI 350
 121 LNFMGASFKNYVMVKYKGSRQRQSVEEFPDSEGPTEPTSTSI 350

Db 301 ILYVFMGASFKNYVMVKYKGSRQRQSVEEFPDSEGPTEPTSTSI 350
 301 ILYVFMGASFKNYVMVKYKGSRQRQSVEEFPDSEGPTEPTSTSI 350

RESULT 13
 AAB37788

ID AAB37788 standard; Protein: 350 AA.

XX AC AAB37788;

XX DT 23-FEB-2001 (first entry)

DE Human TSC7.

XX Human; TSC: tubercous sclerosis complex; cyostatic; antimicrobial; osteopathic; antiulcer; antiasthmatic; antiallergic; neuroprotective; cardiotonic; hypotensive; hypertensive; hortropic; anticonvulsant; analgesic; tranquiliser; immunosuppressive; antiinflammatory; gene therapy; TSC7: infection; cancer; autoimmune disorder; Parkinson's disease; osteoporosis; neurological disorder; Homo sapiens.

XX PN WO200064941-A2.

XX ID AAY57289

PD 02-NOV-2000.

XX PR 20-APR-2000; 2000US-0556002.

XX PA (CURA-) CURAGEN CORP.

XX PI Gould-Rothberg BE;

XX DR WPI; 2000-679670/66.

DR N-PSDB; AAC68722.

XX PN Novel nucleic acid encoding G-protein coupled receptor for diagnosis and treatment of conditions associated with disorder in a G-protein

PT mediated pathway such as cancer, neurological disorders and infections
 PT -
 XX Claim 12; Page 8; 132pp; English.

XX SQ Sequence 350 AA;

Query Match 99.4%; Score 1808; DB 21; Length 350;
 Best Local Similarity 99.4%; Pred. No. 3.3e-194; Matches 348; Conservative 1; Indels 0; Gaps 0; Mismatches 1; Associated with the disorder in a G-protein mediated pathway. They are
 QY 1 MALEQNOSTDYVYENEMGTYDYSQELYCICKEDVREFAKVFLPVFLTVFVIGLAGNS 60
 1 MALEQNOSTDYVYENEMGTYDYSQELYCICKEDVREFAKVFLPVFLTVFVIGLAGNS 60

Db 61 MVAIAYKKORTKTDVYLNLAVADLLFLPFWAVNAVHGVWLGKIMCKTSALYT 120
 61 MVAIAYKKORTKTDVYLNLAVADLLFLPFWAVNAVHGVWLGKIMCKTSALYT 120

Db 121 LNFMGASFKNYVMVKYKGSRQRQSVEEFPDSEGPTEPTSTSI 350
 121 LNFMGASFKNYVMVKYKGSRQRQSVEEFPDSEGPTEPTSTSI 350

Db 301 ILYVFMGASFKNYVMVKYKGSRQRQSVEEFPDSEGPTEPTSTSI 350
 301 ILYVFMGASFKNYVMVKYKGSRQRQSVEEFPDSEGPTEPTSTSI 350

RESULT 14
 AAY57289

ID AAY57289 standard; Protein: 333 AA.

XX AC AAY57289;

XX DT 05-JUN-2000 (first entry)

DE Human BGCKR partial amino acid sequence.

XX Becker Protein; G-protein coupled receptor; human; chemokine; exocytosis; cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV; anti-allergic; antiviral.

XX OS Homo sapiens.

XX PN WO9952945-A2.

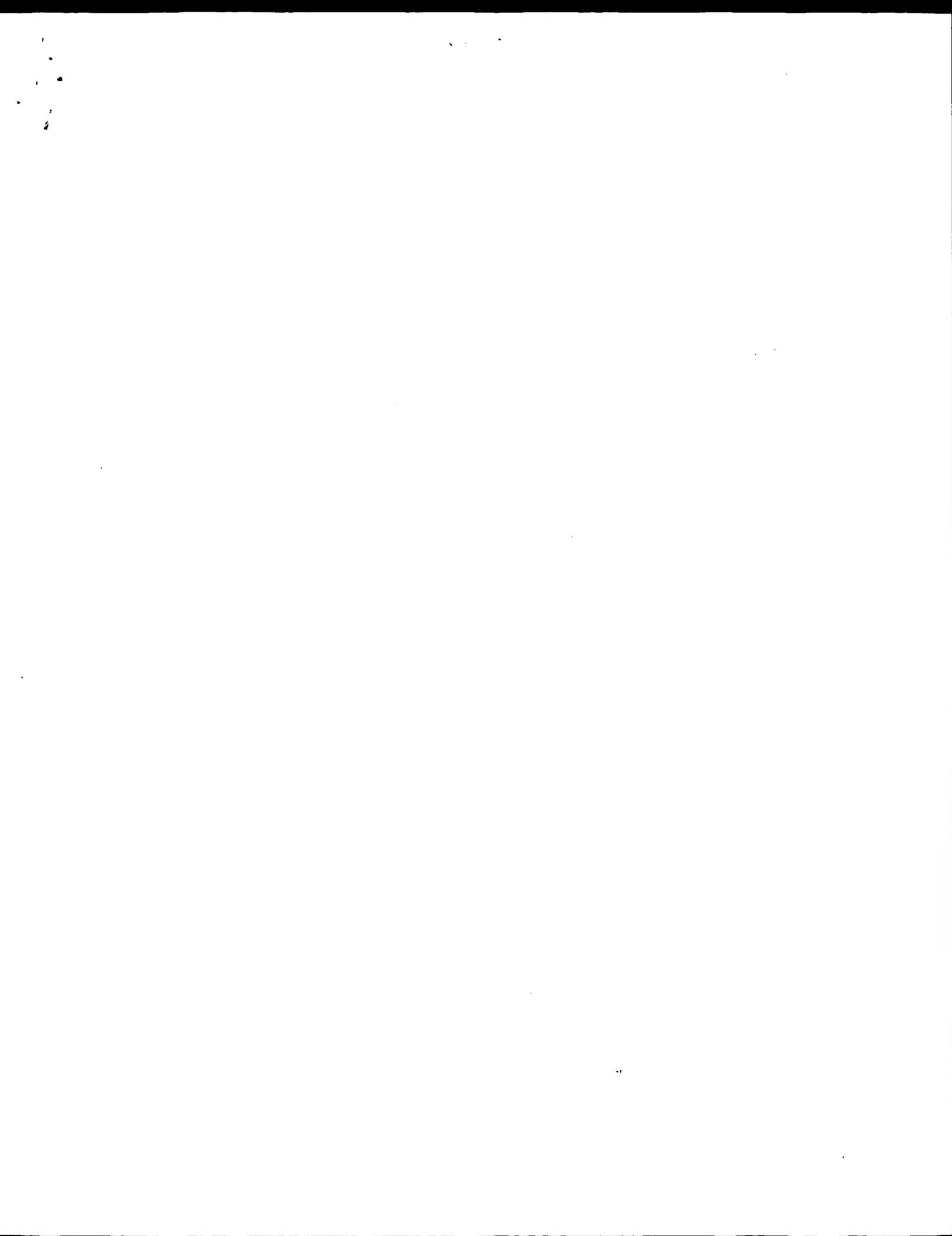
XX PD 21-OCT-1999.

XX 16-APR-1999; 99WO-US08395.
 XX PR 16-APR-1998; 98US-0061153.
 XX PR 16-APR-1999; 99US-0061153.
 XX PA (MILL-) MILLENIUM PHARM INC.
 XX PT Gonzalez JA, Gutierrez-Ramos JC;
 XX PS WPI; 1999-620375/53.
 XX DR N-PSDB; AAZ90527.
 XX PT New nucleic acid encoding human BCCR receptor, used e.g. for
 PT modulating inflammation and tumor growth -
 XX Claim 1; Fig 1A-B; 123pp; English.
 XX The invention relates to a human BCCR protein, a G-protein coupled
 CC receptor. The BCCR protein can be expressed by standard recombinant
 CC methodology. BCCR are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines; cell
 CC proliferation, migration, adhesion and targeting, and exocytosis. The
 CC BCCR nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC tumour growth; allergic reactions and entry of human immune deficiency
 CC virus into cells, for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug screening assays. The present sequence
 CC represents the sequence of a partial human BCCR protein.
 XX Sequence 333 AA;
 XX Query Match 95.0%; score 1728; DB 20; Length 333;
 CC Best Local Similarity 100.0%; Pred. No. 3e-185; Mismatches 0; Indels 0; Gaps 0;
 CC Matches 333; Conservative 0; Mismatches 0;
 CC QY 18 MNGTYDYSQVELICKEDREFAEKVFLPVLTIVFVLAGNSMVATAYKKORTKD 77
 CC 1 MNGTYDYSQVELICKEDREFAEKVFLPVLTIVFVLAGNSMVATAYKKORTKD 60
 CC Db 78 YVILNLAVADLFLFLPFWAVNAVHGWGKIMCKITSALYTINFSGMQFLACISDR 137
 CC 61 YVILNLAVADLFLFLPFWAVNAVHGWGKIMCKITSALYTINFSGMQFLACISDR 120
 CC Db 138 YVAVTKVPSQSGVGKPCWICFCVWMAAILSLIPOLVYTFNDNARCIPIFPRLGTSK 197
 CC 121 YVAVTKVPSQSGVGKPCWICFCVWMAAILSLIPOLVYTFNDNARCIPIFPRLGTSK 180
 CC QY 198 ALIOMLEBICIGFVPLIMGVCFYPTARTLMKMPNIKISPLKVLTVVVFYVOLPN 257
 CC 181 ALIQMЛЕBICIGFVPLIMGVCFYPTARTLMKMPNIKISPLKVLTVVVFYVOLPN 240
 CC Db 258 IVKFCRAIDTYSLLTSCNMNSKRMDIAQTTESTALFHSCLNPLPYVFGKAFKNYVMK 317
 CC 241 IVKFCRAIDTYSLLTSCNMNSKRMDIAQTTESTALFHSCLNPLPYVFGKAFKNYVMK 300
 CC QY 318 AKYGSRQRQSVVEPPFSEGPTEPTFSI 350
 CC 301 AKKYGSWRQRQSVVEPPFSEGPTEPTFSI 333
 CC RESULT 15
 ID AAG67238
 ID AAG67238 standard; Protein: 350 AA.
 AC AAG67238;
 AC XX
 DT 13-NOV-2001 (first entry)
 DE Amino acid sequence of bovine chemokine receptor CCR11.
 XX KW , Human; chemokine receptor; CCR11; G protein coupled receptor;
 XX KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
 KW asthma; angiogenesis; arterosclerosis vascular association disease;
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
 KW left ventricular diastolic dysfunction; migraine; preterm labour;
 KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
 KW myocardial infarction; congestive heart failure; endometriosis;
 KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
 XX OS Bos sp.
 XX PN WO200166598-A2.
 XX DR 13-SEP-2001.
 XX PD 05-MAR-2001; 2001WO-US07073.
 XX PI Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;
 XX PR 03-MAR-2000; 2000US-0186928.
 XX DR WPI; 2001-541918/60.
 XX DR N-PSDB; AAH7712.
 XX PA (ICOS-) ICOS CORP.
 XX PS Example 1; Page 99-100; 110pp; English.
 XX CC The present sequence represents the bovine chemokine receptor CCR11.
 CC CR11 is a member of the G protein coupled receptor family. A CCR11
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
 CC expression or biological activity, is useful for treating many inflammatory
 CC diseases, for example, rheumatoid arthritis, inflammatory
 CC bowel disease, and asthma. They are also useful for treating
 CC angiogenesis, arteriosclerosis vascular association diseases which may
 CC include but are not limited to hypertension, angina pectoris, cardiac
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive
 CC heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or
 CC pulmonary vascular disease.
 XX SQ Sequence 350 AA;
 XX Query Match 89.1%; Score 1620; DB 22; Length 350;
 CC Best Local Similarity 86.0%; Pred. No. 4 2e-173;
 CC Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;
 CC QY 1 MALEQNQSDYYEENENGTYDYSQVELICKEDREFAEKVFLPVLTIVFVLAGNS 60
 CC 1 MAYEQNQSDYYEENENGTYDYSQVELICKEDREFAEKVFLPVLTIVFVLAGNS 60
 CC Db 1 MAVEYNQSDYYEENENGTYDYSQVELICKEDREFAEKVFLPVLTIVFVLAGNS 60
 CC QY 61 MVVAIAYVKQRKTQTVYLNLAVADLFLFLPFWAVNAVHGWGKIMCKITSALYT 120
 CC 61 TVVAIAYVKRKTKTQTVYLNLAVADLFLFLPFWAVNAVHGWGKIMCKITSALYT 120
 CC QY 121 LNFSGMQFLACISDRIVKAVTKVPSQSGVGKPCWICFCVWMAAILSLIPOLVYTFND 180
 CC 121 VNFVSGMQLFLACISTDRIVKAVTKVPSQSGVGKPCWICFCVWMAAILSLIPOLVYTFNVH 180
 CC QY 181 NARCIPIFPRLGTSMALLQMLEICGFVPLIMGVCFYPTARTLMKMPNIKISPLK 240
 CC 181 KARCVPIFPYHGTSMASIQLEICGFVPLIMGVCFYPTARTLMKMPNIKISPLK 240
 CC Db 241 VLLTVVIVFVTFOLPNVVKCRAIDIYSLTSCNMNSKRMDIAQTTESTALFHSCLN 300
 CC DE 241 VLLTVVIVFVTFOLPNVVKCRAIDIYSLTDCDMSKRMVIAQTTESTALFHSCLN 300
 CC Db

• Mon. Mar 17 12:24:54 2003

Qy 301 ILLVNGASKNYVMKVAKKGWSRQRROSVEIPFDSSGPTPEPTSTFSI 350
;||||| ||||:|||||:|||||:||| :||| :||| :||| :||| :||| :|||
Db 301 VLYVFMGTSEKNYIMKVAKKGWSRQRQNVEIPFESEDATEPTSTFSI 350

Search completed: March 14, 2003, 16:11:25
Job time : 38 secs



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Om protein - protein search, using sw model

Run on:

March 14, 2003, 16:09:57 ; Search time 15 Seconds

Perfect score: 1819
 Sequence: 1 MALEQNQSTDYYENEMNG..... VEEFFFDSEGTEPHTSTFSTI 350

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents_AA:
 1: /cgn2_6/ptodata/2/1aa/5A_COMB_pep:
 2: /cgn2_6/ptodata/2/1aa/5B_COMB_pep:
 3: /cgn2_6/ptodata/2/1aa/6A_COMB_pep:
 4: /cgn2_6/ptodata/2/1aa/6B_COMB_pep:
 5: /cgn2_6/ptodata/2/1aa/PCITS_COMB_pep:
 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1819	100.0	350	2 US-08-966-316-16
2	1620	89.1	350	2 US-08-966-316-18
3	659	36.2	358	1 US-08-153-848-19
4	659	36.2	358	3 US-09-884-843A-19
5	659	36.2	358	4 US-09-088-337B-19
6	659	36.2	358	5 PCT-US93-11153-19
7	659	36.2	378	1 US-08-848-15
8	659	36.2	378	3 US-09-299-843A-15
9	659	36.2	378	4 US-09-251-545-1
10	659	36.2	378	4 US-09-843A-15
11	659	36.2	378	5 PCT-US93-11153-15
12	659	36.2	410	1 US-08-153-848-7
13	659	36.2	410	3 US-08-299-843A-7
14	659	36.2	410	4 US-09-088-337B-7
15	659	36.2	410	5 PCT-US93-11153-7
16	650	35.7	378	4 US-09-299-843A-66
17	650	35.7	378	4 US-09-088-337B-66
18	643	35.3	378	1 US-08-383-750-2
19	643	35.3	378	1 US-08-299-843A-2
20	643	35.3	378	3 US-08-352-678-2
21	643	35.3	378	4 US-09-045-583-49
22	643	35.3	378	4 US-09-534-185-49
23	643	35.3	378	5 PCT-US93-09636-2
24	637	35.0	357	4 US-09-266-464-2
25	635.5	34.9	359	1 US-08-153-848-24
26	635.5	34.9	359	3 US-09-299-843A-24
27	635.5	34.9	359	4 US-09-088-337B-24

ALIGNMENTS

RESULT 1
 US-08-966-316-16
 Sequence 16, Application US/08966316
 Patent No. 5932445
 GENERAL INFORMATION:
 APPLICANT: Lal, Preeti
 APPLICANT: Au-Young, Janice
 APPLICANT: Reddy, Roopa
 APPLICANT: Murty, Lynn E.
 APPLICANT: Mathur, Preete
 TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/966,316
 FILING DATE: Herewitz
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0424 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: UTRSN011
 CLONE: 2547002
 US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.7e-147; Matches 350; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 MALEQNOSTDYYEENEMNTYDYSOELTICKEDVREFAKVFLPFLTVFVLAGNS 60
 Db 1 MALEQNOSTDYYEENEMNTYDYSOELTICKEDVREFAKVFLPFLTVFVLAGNS 60
 Qy 61 MVVAIAYYKORTKDVTLYNLAVALDILFLTPFWAVNAVIGWLGKIMCKITSALYT 120
 Db 61 MVVAIAYYKORTKDVTLYNLAVALDILFLTPFWAVNAVIGWLGKIMCKITSALYT 120
 Qy 181 NARCIPIFPRLGTSKALIQMELICIGFWPLFLMGCVYFITARTLMPNPKSRPLK 240
 Db 181 NARCIPIFPRLGTSKALIQMELICIGFWPLFLMGCVYFITARTLMPNPKSRPLK 240
 Qy 241 VLTVVIVFVTLQPNYTKFCRAIDIYSLTSNCMSKRMIDAIQVTEIAFHSCLN 300
 Db 241 VLTVVIVFVTLQPNYTKFCRAIDIYSLTSNCMSKRMIDAIQVTEIAFHSCLN 300
 Qy 301 ILYVFMGASKNYIMKVKYGSWRQRROSVEEPESEGPTPTPSI 350
 Db 301 ILYVFMGASKNYIMKVKYGSWRQRROSVEEPESEGPTPTPSI 350

RESULT 2
 US-09-966-316-18
 Sequence 18, Application US/08966316
 Patent No. 5932445
 GENERAL INFORMATION:
 APPLICANT: Lal, Preeti
 APPLICANT: Au-Yong, Janice
 APPLICANT: Ruddy, Roopa
 APPLICANT: Murry, Lynn E.
 APPLICANT: Mathur, Preeta
 TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 COMPUTER TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEE FOR windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/966,316
 FILING DATE: Herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0424 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEX: 650-845-4166

INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

Query Match 89.1%; Score 1620; DB 2; Length 350;
 Best Local Similarity 86.0%; Pred. No. 1.4e-130; Matches 301; Conservative 27; Mismatches 22; Gaps 0; Indels 0;

Qy 1 MALEQNOSTDYYEENEMNTYDYSOELTICKEDVREFAKVFLPFLTVFVLAGNS 60
 Db 1 MAVENOSTDYYEENEMNTYDYSOELTICKEDVREFAKVFLPFLTVFVLAGNS 60
 Qy 61 MVVAIAYYKORTKDVTLYNLAVALDILFLTPFWAVNAVIGWLGKIMCKITSALYT 120
 Db 61 MVVAIAYYKORTKDVTLYNLAVALDILFLTPFWAVNAVIGWLGKIMCKITSALYT 120
 Qy 181 NARCIPIFPRLGTSKALIQMELICIGFWPLFLMGCVYFITARTLMPNPKSRPLK 240
 Db 181 NARCIPIFPRLGTSKALIQMELICIGFWPLFLMGCVYFITARTLMPNPKSRPLK 240
 Qy 241 VLTVVIVFVTLQPNYTKFCRAIDIYSLTSNCMSKRMIDAIQVTEIAFHSCLN 300
 Db 241 VLTVVIVFVTLQPNYTKFCRAIDIYSLTSNCMSKRMIDAIQVTEIAFHSCLN 300
 Qy 301 ILYVFMGASKNYIMKVKYGSWRQRROSVEEPESEGPTPTPSI 350
 Db 301 ILYVFMGASKNYIMKVKYGSWRQRROSVEEPESEGPTPTPSI 350

RESULT 3
 US-08-153-848-19
 Sequence 19, Application US/08153848
 Patent No. 5759804
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schweikart, Vicki L.
 TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/153,848
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452
 FILING DATE: 17-Nov-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5759804and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-0418
 TELEX: 25-3856

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/088,337B
 FILING DATE: 01-Jun-1998
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: No 6348574 and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 MOLECULE TYPE: protein
 TOPOLGY: linear
 TYPE: amino acid
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-088-337B-19

Query Match 36.2%; Score 659; DB 4; Length 358;
 Best Local Similarity 38.7%; Pred. No. 9.7e-49; Mismatches 144; Indels 38; Gaps 7; Matches 144; Conservative 66; MisMatches 124; Del 38; Gaps 7;

QY 1 MALEQNQSTDYVYENEMNGTVDSQYELICKEDVREFAKVFLPVLTIVVIGLAGNS 60
 : || | : || | : || | : || | : || | : || | : || | : || | : || |
 Db 1 VCLQDQEVDYDDYGDNT--TVDYTLFESLCSKDKVRNFKANFLPIMYSICFVGULGNG 57

QY 61 MVVAIAYVYKKORTKTDYVILNAVADILFLPFWAVNAVHGGWIGRKIMCKITSALYT 120
 : || | : || | : || | : || | : || | : || | : || | : || | : || |
 Db 58 LVLVITYVYFKRLKMTDYLNLNAVADILFLPFWAVSAAKSWWFGVHFCKLIFAYK 117

QY 121 LNFVSGMQLACISIDRYVATVKPS---QSGVGKPCWICFCVWMAAILISIPOLQFY 176
 : || | : || | : || | : || | : || | : || | : || | : || |
 Db 118 MSFSGMLLCLCISIDRYVAVSAHRARVLLSKLSCVGWIATVLSIPELLYS 177

QY 177 TVNDNA---RCIPIFFRGLGTSMKALIQMLEICIGFWFPLIMGCVFTARTLKKMP 231
 : || | : || | : || | : || | : || | : || | : || | : || |
 Db 178 DLQRSSSEQAMRCSLITEH--VFAFTIQVAMWIGFLVPLAMSCYLVIRTLQAR 234

QY 232 NIKISRPKVLVTVVIVTQPLYNTVKCRAIDIYSLTSNCNSMRMDIAQVTESTI 291
 : || | : || | : || | : || | : || | : || | : || | : || |
 Db 235 NFERNAKAIVKVIAVVVVFQFQLYINGVLAQTVANFNITSSCIELSKOLNIAYDVYSL 294

QY 292 ALFHSCNPLVFMGASFKNYVMVKYKG-----SW-----RRQROSVEEFPFD 337
 : || | : || | : || | : || | : || | : || | : || |
 Db 295 ACVRCCVNPFLAFIGVKFRNDLFLKFLRGCLSQEQLROWSSCRHIRRSSMSVE--- 349

QY 338 SEGPTEPSTS 349
 : || | : || | : || | : || | : || | : || |
 Db 350 ---AETTTFS 357

RESULT 6
 PCT-US93-1153-19
 ; Sequence 19, Application PC/TUS9311153
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schweikart, Vicki L.
 ; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/11153
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 MOLECULE TYPE: protein
 TOPOLGY: linear
 TYPE: amino acid
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-088-337B-19

Query Match 36.2%; Score 659; DB 5; Length 358;
 Best Local Similarity 38.7%; Pred. No. 9.7e-49; Mismatches 144; Indels 38; Gaps 7; Matches 144; Conservative 66; MisMatches 124; Del 38; Gaps 7;

QY 1 MALEQNQSTDYVYENEMNGTVDSQYELICKEDVREFAKVFLPVLTIVVIGLAGNS 60
 : || | : || | : || | : || | : || | : || | : || |
 Db 1 VCLQDQEVDYDDYGDNT--TVDYTLFESLCSKDKVRNFKANFLPIMYSICFVGULGNG 57

QY 61 MVVAIAYVYKKORTKTDYVILNAVADILFLPFWAVNAVHGGWIGRKIMCKITSALYT 120
 : || | : || | : || | : || | : || | : || | : || |
 Db 58 LVLVITYVYFKRLKMTDYLNLNAVADILFLPFWAVSAAKSWWFGVHFCKLIFAYK 117

QY 121 LNFVSGMQLACISIDRYVATVKPS---QSGVGKPCWICFCVWMAAILISIPOLQFY 176
 : || | : || | : || | : || | : || | : || | : || |
 Db 118 MSFSGMLLCLCISIDRYVAVSAHRARVLLSKLSCVGWIATVLSIPELLYS 177

QY 177 TVNDNA---RCIPIFFRGLGTSMKALIQMLEICIGFWFPLIMGCVFTARTLKKMP 231
 : || | : || | : || | : || | : || | : || | : || |
 Db 178 DLQRSSSEQAMRCSLITEH--VFAFTIQVAMWIGFLVPLAMSCYLVIRTLQAR 234

QY 232 NIKISRPKVLVTVVIVTQPLYNTVKCRAIDIYSLTSNCNSMRMDIAQVTESTI 291
 : || | : || | : || | : || | : || | : || | : || |
 Db 235 NFERNAKAIVKVIAVVVVFQFQLYINGVLAQTVANFNITSSCIELSKOLNIAYDVYSL 294

QY 292 ALFHSCNPLVFMGASFKNYVMVKYKG-----SW-----RRQROSVEEFPFD 337
 : || | : || | : || | : || | : || | : || |
 Db 295 ACVRCCVNPFLAFIGVKFRNDLFLKFLRGCLSQEQLROWSSCRHIRRSSMSVE--- 349

QY 338 SEGPTEPSTS 349
 : || | : || | : || | : || | : || |
 Db 350 ---AETTTFS 357

RESULT 7
 US-08-153-848-15
 ; Sequence 15, Application US/08153848
 ; Patent No. 575904
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.
 APPLICANT: Schweikart, Vicki L.
 TITLE OF INVENTION: No. 5755804el Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5759804and, Greta E.

PRIOR APPLICATION DATA:
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 378 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-153-848-15

Query Match 36.2%; Score 659; DB 1; Length 378;
 Best Local Similarity 38.7%; Pred. No. 1e-48;
 Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

Qy 1 MALEQNQSTDYEEENEMNTYDYSQVELICKEDVREFAKVFLPFLTIVFVLAGNS 60
 Db 21 VLCODEVTDDYIGDT--TVDTLFESLCKSKDVRFNFKAWFLPIMSIICHVGLGNG 77
 Qy 61 MWVATIAYYKKQRDKRDKVYILNAVADILFLTPFWAVNAVHWGWLKGKMCITSALYT 120
 Db 78 LVVLTYYFFKRKLTMDTYLLNLAVALDILFLTPFWAVSAAKSWWFGVHFCRKLIAYK 137
 Qy 121 LNFGSGMQFLACISIDRYWAVTKVPS---QSGVKPCWICFCVWMAILLSPOLVFY 176
 Db 138 MSFFSGMLLICISIDRYVAVQSAHRRAVLLISKSCVGIVIATVLISIPELLYS 197
 Qy 177 TVNDNA---RCPIPIPRYLGTSMKALIQMLEICIGFVWPFLPFLMVGYFTARTLMKP 231
 Db 198 DLQRSSSEQAMRCSLITEH--VEAFITQAVQHGVFLPFLAMSFCVLYIRTLLQAR 254
 Qy 232 NIKISPLKVLVTVVTFVLPNIVKFCRADITYSITSNCNSKRDIAQVTESI 291
 Db 255 NFERNAKAIKVIAVVVVFIVFOLPQNGVVAQTVANFNITSSTCSELSKOLNIADVTLS 314
 Qy 292 ALFHSCNPLTYFVFGASFKNYVMVKAKYGG-----SW----RQROVVEEFPD 337
 Db 315 ACVRCCCNPFYLAFTGKFRNDFKLKDGLCSQEQLROWSSCRHIRSMSVE---- 369
 Qy 338 SEGPTEPTSF 349
 Db 370 ---AEWTTEFS 377

RESULT 8
 US-09-299-843A-15

/ Sequence 15, Application us-09299843A
 / Patent No. 6107475
 / GENERAL INFORMATION:
 / APPLICANT: Godiska, Ronald
 / APPLICANT: Gray, Patrick W.
 / APPLICANT: Schweikart, Vicki L.
 / TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
 / NUMBER OF SEQUENCES: 66
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 / STREET: 6300 Sears Tower, 233 South Wacker Drive
 / CITY: Chicago
 / STATE: Illinois
 / COUNTRY: USA
 / ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 FILING DATE: 01-JUN-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: J11E. Uhl

PRIOR APPLICATION DATA:
 REGISTRATION NUMBER: US 09/088, 337
 REFERENCE/DOCKET NUMBER: 27666/32059B
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 378 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-153-848-15

Query Match 36.2%; Score 659; DB 3; Length 378;
 Best Local Similarity 38.7%; Pred. No. 1e-48;
 Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

Qy 1 MALEQNQSTDYEEENEMNTYDYSQVELICKEDVREFAKVFLPFLTIVFVLAGNS 60
 Db 21 VLCODEVTDDYIGDT--TVDTLFESLCKSKDVRFNFKAWFLPIMSIICHVGLGNG 77
 Qy 61 MWVATIAYYKKQRDKRDKVYILNAVADILFLTPFWAVNAVHWGWLKGKMCITSALYT 120
 Db 78 LVVLTYYFFKRKLTMDTYLLNLAVALDILFLTPFWAVSAAKSWWFGVHFCRKLIAYK 137
 Qy 121 LNFGSGMQFLACISIDRYWAVTKVPS---QSGVKPCWICFCVWMAILLSPOLVFY 176
 Db 138 MSFFSGMLLICISIDRYVAVQSAHRRAVLLISKSCVGIVIATVLISIPELLYS 197
 Qy 177 TVNDNA---RCPIPIPRYLGTSMKALIQMLEICIGFVWPFLPFLMVGYFTARTLMKP 231
 Db 21 VLCODEVTDDYIGDT--TVDTLFESLCKSKDVRFNFKAWFLPIMSIICHVGLGNG 77
 Qy 61 MWVATIAYYKKQRDKRDKVYILNAVADILFLTPFWAVNAVHWGWLKGKMCITSALYT 120
 Db 78 LVVLTYYFFKRKLTMDTYLLNLAVALDILFLTPFWAVSAAKSWWFGVHFCRKLIAYK 137
 Qy 121 LNFGSGMQFLACISIDRYWAVTKVPS---QSGVKPCWICFCVWMAILLSPOLVFY 176
 Db 138 MSFFSGMLLICISIDRYVAVQSAHRRAVLLISKSCVGIVIATVLISIPELLYS 197
 Qy 177 TVNDNA---RCPIPIPRYLGTSMKALIQMLEICIGFVWPFLPFLMVGYFTARTLMKP 231
 Db 198 DLQRSSSEQAMRCSLITEH--VEAFITQAVQHGVFLPFLAMSFCVLYIRTLLQAR 254
 Qy 232 NIKISPLKVLVTVVTFVLPNIVKFCRADITYSITSNCNSKRDIAQVTESI 291

Page 6

QY 338 SEGPTEPTSTFS 349
 PCT-US93-11153-15
 Sequence 15, Application PC/TUS9311153
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schweikart, Vicki L.
 TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 ZIP: 60606
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/TUS93/11153
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452
 FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEX: 25 3856
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 378 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 PCT-US93-11153-15

Query Match 36.2%; Score 659; DB 5; Length 378;
 Best Local Similarity 38.7%; Pred. No. 1.e-48;
 Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSTDYVYENEMGTYDSQVELCICEDVERAKFVFLVFLTVFVIGLAGNS 60
 DB 21 VCLCQDEVTDDYIGDNT--TVDYTLEFESLCSKKDKVRNFKAWFLPIMYSICFGVLGNG 77
 QY 61 MVVAVIAYKKRKTQDVTYILNLAVALDLFLTPFWAVWAVHGVGLKIMCKITSALVT 120
 DB 78 IIVLVITYFKRLKTMIDYLNLNAVALDILFLTPFWAVSAKSWSVFGVHFKLFAIK 137
 QY 121 LNFGVSGMQLFLACISIDRYAVTKVPS---QSGVSKPCWICFCVWMATLSPOLVY 176
 DB 138 MSFFSGMLLCLCISIDRYAVIAVSAHRHRARVLTSKLSCVGWIWATLVSPIPELVS 197
 QY 177 TVNDA---RCIPPFPRYLGTSMKALIQMELIGFWFLPGVCFITARTLMKP 231
 DB 198 DQRSSEQAMRCSLITEH--VERAFITQVAQOMVIGFLYPLAMSPCYLVIIRPLQ 254
 QY 232 NKISRPLKVLTWVIVFVTPOLPYNUVKFCRADIYTSLTSCHNSMRKDIATQVTESTI 291
 DB 255 NERNKAIVKIVAVVVVFVQDPLPQVWVLAQTVANFNITSSCIELSKQNLNIAIDVYSL 314

QY 292 ALFHSCLNPLIVYMGASFKKNYMKVAKKG-----SW-----RRQRQSVEFPFD 337
 Db 315 ACYRCVNEFLKAFIGVKFRNDLFKLKDGLSQQLRQWSSCRHRRSSMSVE---- 369
 QY 338 SEGPTEPTSTFS 349
 PCT-US93-11153-15
 Sequence 7, Application US/08153848
 PATENT NO. 5759804
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schweikart, Vicki L.
 TITLE OF INVENTION: NO. 5759804el Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/153,848
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452
 FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 5759804 and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEX: (312) 474-0448
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 OS-08-153-848-7

Query Match 36.2%; Score 659; DB 1; Length 410;
 Best Local Similarity 38.7%; Pred. No. 1.e-48;
 Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSTDYVYENEMGTYDSQVELCICEDVERAKFVFLVFLTVFVIGLAGNS 60
 DB 53 VCLCQDEVTDDYIGDNT--TVDYTLEFESLCSKKDKVRNFKAWFLPIMYSICFGVLGNG 109
 QY 61 MVVAVIAYKKRKTQDVTYILNLAVALDLFLTPFWAVWAVHGVGLKIMCKITSALVT 120
 DB 78 IIVLVITYFKRLKTMIDYLNLNAVALDILFLTPFWAVSAKSWSVFGVHFKLFAIK 137
 QY 121 LNFGVSGMQLFLACISIDRYAVTKVPS---QSGVSKPCWICFCVWMATLSPOLVY 176
 DB 138 MSFFSGMLLCLCISIDRYAVIAVSAHRHRARVLTSKLSCVGWIWATLVSPIPELVS 197
 QY 177 TVNDA---RCIPPFPRYLGTSMKALIQMELIGFWFLPGVCFITARTLMKP 231
 DB 198 DQRSSEQAMRCSLITEH--VERAFITQVAQOMVIGFLYPLAMSPCYLVIIRPLQ 254
 QY 232 NKISRPLKVLTWVIVFVTPOLPYNUVKFCRADIYTSLTSCHNSMRKDIATQVTESTI 291
 DB 255 NERNKAIVKIVAVVVVFVQDPLPQVWVLAQTVANFNITSSCIELSKQNLNIAIDVYSL 314

QY 177 TVNDA---RCIPPFPRYLGTSMKALIQMELIGFWFLPGVCFITARTLMKP 231

RESULT 13
 US-09-299-843A-7
 Sequence 7, Application US/09299843A
 Patent No. 610745
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schweikart, Vicki L.
 TITLE OF INVENTION: No. 610745el Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/299,843A
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 09/088,337
 FILING DATE: 01-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/153,848
 FILING DATE: 17-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Jill E. Uhl
 REGISTRATION NUMBER: 43,213
 REFERENCE/DOCKET NUMBER: 27866/32059B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX:
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-299-843A-7

Query Match 36.2%; Score 659; DB 3; Length 410;
 Best Local Similarity 38.7%; Pred. No. 1.e-48;
 Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNQSTIYVYENEMNGTYDYSQEVICLKIDVRERAKVLPVFLTIVFVGLAGNS 60

RESULT 14
 US-09-088-337B-7
 Sequence 7, Application US/09088337B
 Patent No. 634574
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schweikart, Vicki L.
 TITLE OF INVENTION: No. 634574el Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/088,337B
 FILING DATE: 01-Jun-1998
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/153,848
 FILING DATE: 17-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Greta E. E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 311794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX:
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 410 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

QY 53 VLCQCODEVDVYIGDN-----TVDYTLIFESLCSRKDVYRNFKAWFLPIMYSTICFGVLGNG 109
 QY 61 MVVAIAYAKKKQRTKTDVILNIAVADLLFLTPFWANAVHGWLGKMCMTSALYT 120
 Db 110 LNFVSGMQLACTSIDRVAVTRVP-----RRQRQSVEFPFD 337
 Db 121 LNFVSGMQLACTSIDRVAVTRVP-----RRQRQSVEFPFD 337
 Db 110 LNFVSGMQLACTSIDRVAVTRVP-----RRQRQSVEFPFD 337
 Db 170 MSFFGMLLCLCISIDRVAVIQAWSAHRRAVRLLISKSCVGIVILAVLISBELYS 229
 QY 338 SEGTEPTSTS 349
 QY 177 TVIDNA----RCPIPFRPLGTSMKALIOMEICIGFVVERFLIMCVCYTARTLKMPC 231
 Db 230 DLRSSEQAMRCSLTEH---VEAFITIQAQMVIGFLVPLAMSFCYLVIRTLQAR 286
 QY 232 NIKTSRPLKVLTVWIFLQPLPNVKFCRAIDIYSLTSCNMSKRMIDIAOTEST 291
 Db 287 NFERNAKAIVTIAVWVFLVQFOLPVLAQTVNFTNTSSTCELSKQNIAYDVTSL 346
 QY 292 ALFHSCLNPLIVFMGASFKNVVMKVAKKG-----SW-----RRQRQSVEFPFD 337
 Db 347 ACVRCCVNPFLYAFIGVKFRNDLFKLFKDIQCLSQBLQRLWSSCRHIRSSMSVB---- 401
 QY 338 SEGTEPTSTS 349
 Db 402 ---AEFTTTF 409



GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw mode..

Run on: March 14, 2003, 16:12:17 ; Search time 14 Seconds
 (without alignments) (without alignments)

Title: US-09-686-020a-2

Perfect score: 1819

Sequence: 1 MALEQNSTDYEEENMNG... VEEFPFDSEGPTPEPTSTFSI 350

Scoring table: BLOSUM62

gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA:*

1: /egn2_6/ptodata/2/pubpea/US08_NEW_PUB.pep: *
 2: /cn2_6/ptodata/2/pubpea/PCT_NEW_PUB.pep: *
 3: /cn2_6/ptodata/2/pubpea/US06_PUBCOMB.pep: *
 4: /cn2_6/ptodata/2/pubpea/US06_PUBCOMB.pep: *
 5: /cn2_6/ptodata/2/pubpea/US07_PUBCOMB.pep: *
 6: /cn2_6/ptodata/2/pubpea/US07_PUBCOMB.pep: *
 7: /cn2_6/ptodata/2/pubpea/PCTCOMB.pep: *
 8: /cn2_6/ptodata/2/pubpea/US08_PUBCOMB.pep: *
 9: /cn2_6/ptodata/2/pubpea/US09_PUBCOMB.pep: *
 10: /egn2_5/ptodata/2/pubpea/US10_NEW_PUB.pep: *
 11: /egn2_5/ptodata/2/pubpea/US10_PUBCOMB.pep: *
 12: /egn2_6/ptodata/2/pubpea/US10_PUBCOMB.pep: *
 13: /egn2_6/ptodata/2/pubpea/US60_NEW_PUB.pep: *
 14: /egn2_6/ptodata/2/pubpea/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
 US-09-765-994-2
 ; Sequence 2, Application US/09765994
 ; Patent NO US2001016336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ELLIS, CATHERINE
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR
 ; TITLE OF INVENTION: (HFIAC041)
 ; FILE REFERENCE: GH-70225-C1
 ; CURRENT APPLICATION NUMBER: US/09-765, 994
 ; CURRENT FILING DATE: 2001-01-19
 ; PRIORITY APPLICATION NUMBER: 60/055, 895
 ; PRIORITY FILING DATE: 1997-08-15
 ; PRIORITY FILING DATE: 1997-10-27
 ; PRIORITY APPLICATION NUMBER: 08/962, 922
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 350
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS

Query Match 100 %; Score 1819; DB 10; Length 350;
 Best Local Similarity 100.0%; Pred. No. 5.7e-153;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEQNSTDYEEENMNGTYDSOYELCICKEDVREFKKVFLPVLTIVFVLAGNS 60
 |||||||...|||||||...|||||||...|||||||...|||||||...|||||||...|||||||...
 Db 1 MALEQNSTDYEEENMNGTYDSOYELCICKEDVREFKKVFLPVLTIVFVLAGNS 60
 |||||||...|||||||...|||||||...|||||||...|||||||...|||||||...|||||||...
 Qy 61 MVVAIYAYKVKORTKTDVYILNLAVADLILFPLPMAWAVHGMVLGKIMCKITSALY 120
 |||||||...|||||||...|||||||...|||||||...|||||||...|||||||...|||||||...
 Db 61 MVVAIYAYKVKORTKTDVYILNLAVADLILFPLPMAWAVHGMVLGKIMCKITSALY 120
 |||||||...|||||||...|||||||...|||||||...|||||||...|||||||...|||||||...
 Qy 121 LNFVSGMOPFLACISIDRVYAVKVPSSGWSKPCWICFCEWMAILLSPLQVLYTVND 180
 |||||||...|||||||...|||||||...|||||||...|||||||...|||||||...|||||||...
 Db 121 LNFSVSGMOPFLACISIDRVYAVKVPSSGWSKPCWICFCEWMAILLSPLQVLYTVND 180
 |||||||...|||||||...|||||||...|||||||...|||||||...|||||||...|||||||...
 Qy 181 NARCIPIPPRYLGTSMALLQMLEICITGFVVFPLFLMGVCYFTTARTLKMENIKSRPL 240
 |||||||...|||||||...|||||||...|||||||...|||||||...|||||||...|||||||...
 Db 181 MARCIPIPRIGLTSKMLQMLEICIGVVFPLFLMGVCYFTTARTLKMENIKSRPL 240

RESULT 2
US-09-796-338A-8
; Sequence 8, Application US/09796338A
; Patent No. US20020061522A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 1983, 5,2881, 2393, 4549, 50289, AND
TITLE OF INVENTION: 5,2872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
FILE REFERENCE: 10448-020001
CURRENT APPLICATION NUMBER: US/09/796, 338A
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/186, 059
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO: 8
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
US-09-796-338A-8

Query Match 100 %; Score 1819; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 5.7e-153;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MALEQNQSTDYEEENEMNGTYDYSQEYELICKEDVREFAKVFLPFLTVFVLAGNS 60
QY 61 MWVAYAYKKORTKDVVYLNLAVADLLLFTLPFWAVNAVHGWLGMCKITSALYT 120
Db 61 MWVAYAYKKORTKDVVYLNLAVADLLLFTLPFWAVNAVHGWLGMCKITSALYT 120
QY 121 LNFGSGMQLACISIDRYVATKPSQSGVKPCWICCVWMAAILSIPOLVFTND 180
Db 121 LNFGSGMQLACISIDRYVATKPSQSGVKPCWICCVWMAAILSIPOLVFTND 180
QY 181 NARCIPIPRVLGTSMKALIQMLETCIGFVVPFLIMGWCYFITARTLMKPNIKSRPLK 240
Db 181 NARCIPIPRVLGTSMKALIQMLETCIGFVVPFLIMGWCYFITARTLMKPNIKSRPLK 240
QY 241 VLTIVVIVFVTOPLPYNIVFCRAIDIYSLITSCNMNSKRMDIAQVTESTIALFHSCLN 300
Db 241 VLTIVVIVFVTOPLPYNIVFCRAIDIYSLITSCNMNSKRMDIAQVTESTIALFHSCLN 300
QY 301 ILYVMGASKNYKVKYKGSMRRQROSVEEFPDSGCPTEPTSTSI 350
Db 301 ILYVMGASKNYKVKYKGSMRRQROSVEEFPDSGCPTEPTSTSI 350

RESULT 3
US-09-765-994-4
; Sequence 4, Application US/09765994
; Patent No. US20010016336A1
GENERAL INFORMATION:
APPLICANT: Ellis, Catherine
TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR
TITLE OF INVENTION: (HFI041)
FILE REFERENCE: GH-70225-CL
CURRENT APPLICATION NUMBER: US/09/765, 994
CURRENT FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/055, 895
PRIOR FILING DATE: 1997-08-15

RESULT 4
US-09-989-442-108
; Sequence 108, Application US/09989442
; Publication No. US20030011649A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PZ08
CURRENT APPLICATION NUMBER: US/09/989, 442
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/179, 065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180, 628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214, 886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217, 487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225, 758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220, 963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217, 496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225, 447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218, 290
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225, 757
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/226, 868
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/216, 647
PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 4
LENGTH: 349
TYPE: PRY
ORGANISM: HOMO SAPIENS
US-09-765-994-4

Query Match 99.7%; Score 1814; DB 10; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.6e-152;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 ALEONQSTDYEEENEMNGTYDYSQEYELICKEDVREFAKVFLPFLTVFVLAGNS 61
QY 62 WAIAYAYKKORTKDVVYLNLAVADLLLFTLPFWAVNAVHGWLGMCKITSALYT 121
Db 61 WAIAYAYKKORTKDVVYLNLAVADLLLFTLPFWAVNAVHGWLGMCKITSALYT 120
QY 122 NFVSGMQLACISIDRYVATKPSQSGVKPCWICCVWMAAILSIPOLVFTND 181
Db 121 NFVSGMQLACISIDRYVATKPSQSGVKPCWICCVWMAAILSIPOLVFTND 180
QY 182 ARCFIPRVLGTSMKALIQMLETCIGFVVPFLIMGWCYFITARTLMKPNIKSRPLK 241
Db 181 ARCFIPRVLGTSMKALIQMLETCIGFVVPFLIMGWCYFITARTLMKPNIKSRPLK 240
QY 242 LLTVVIVFVTOPLPYNIVFCRAIDIYSLITSCNMNSKRMDIAQVTESTIALFHSCLN 301
Db 241 LLTVVIVFVTOPLPYNIVFCRAIDIYSLITSCNMNSKRMDIAQVTESTIALFHSCLN 300
QY 302 ILYVMGASKNYKVKYKGSMRRQROSVEEFPDSGCPTEPTSTSI 350
Db 301 ILYVMGASKNYKVKYKGSMRRQROSVEEFPDSGCPTEPTSTSI 349

PRIOR APPLICATION NUMBER: 08/062, 922
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 4
LENGTH: 349
TYPE: PRY
ORGANISM: HOMO SAPIENS
US-09-765-994-4

PRIOR APPLICATION NUMBER: 60/225, 267
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/216, 880
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225, 270
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/251, 869
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/225, 834
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/234, 274
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/228, 924
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/224, 518
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236, 369
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/224, 519
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220, 964
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/241, 809
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249, 299
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/235, 327
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/241, 785
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249, 299
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/225, 268
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/236, 368
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/251, 856
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/251, 868
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/229, 344
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 60/229, 343
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229, 345
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229, 287
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229, 513
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/231, 413
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/229, 509
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/236, 367
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/237, 039
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237, 038
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/236, 370
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236, 802
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237, 037
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237, 040
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/240, 950
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/249, 216
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 213
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/246, 474
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/241, 787
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249, 210
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/226, 681
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/249, 216
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225, 213
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/227, 182
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/225, 214
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/235, 836
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230, 438
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/215, 135
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/225, 266
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/249, 212
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/215, 135
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PRIOR APPLICATION NUMBER: 60/249, 215
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PRIOR APPLICATION NUMBER: 60/249, 207
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 245
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 215
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 244
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 217
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 211
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 215
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 264
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 214
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232, 081
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232, 080
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231, 242
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231, 241
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231, 244
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231, 244
PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/233,063
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,397
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,399
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,401
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,826
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,065
PRIOR FILING DATE: 2000-09-14

Query Match Best Local Similarity 41.8%; Score 761; DB 9; Length 175;
Matches 148; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 197 KALIOMLEICIGFVWFLIMGVCFITARTLMKMPNIKSRLPKVLTVVIVFTVOLPY 256
Db 22 ESDSMLEICIGFVWFLIMGVCFITERTLMKMPNIKSRLPKVLTVVIVFTVOLPY 81

QY 257 NIVKFCRAIDIYLISLTSNCNSKRMIDAIQVTESIALFHSCLNPILYVFMGASKNYMK 316
Db 82 NIVKFCRAIDIYLISLTSNCNSKRMIDAIQVTESIALFHSCLNPILYVFMGASKNYMK 141

QY 317 VAKKYGSWRQRQSVEEFPDSEGPTEPTSTFSI 350
Db 142 VAKKYGSWRQRQSVEEFPDSEGPTEPTSTFSI 175

RESULT 5 US-10-073-865-91
Sequence 91, Application US10073865
Publication No. US20030044904A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P1001
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US10/073,865
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 91
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (19)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

US-09-966-755-2
Sequence 2, Application US09966755
Publication No. US200302228A1
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponata, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
FILE REFERENCE: LRS98-16
CURRENT APPLICATION NUMBER: US09/966,755
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 2
LENGTH: 357
TYPE: PRT

QY 257 NIVKFCRAIDIYLISLTSNCNSKRMIDAIQVTESIALFHSCLNPILYVFMGASKNYMK 316
Db 82 NIVKFCRAIDIYLISLTSNCNSKRMIDAIQVTESIALFHSCLNPILYVFMGASKNYMK 141

QY 317 VAKKYGSWRQRQSVEEFPDSEGPTEPTSTFSI 350
Db 142 VAKKYGSWRQRQSVEEFPDSEGPTEPTSTFSI 175

RESULT 6 US-09-764-853-584
Sequence 584, Application US/09764853
PATENT NO. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P10206
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 584
LENGTH: 175
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (16)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (19)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

US-09-764-853-584

Query Match Best Local Similarity 41.8%; Score 761; DB 10; Length 175;
Matches 148; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 197 KALIOMLEICIGFVWFLIMGVCFITARTLMKMPNIKSRLPKVLTVVIVFTVOLPY 256
Db 22 ESDSMLEICIGFVWFLIMGVCFITERTLMKMPNIKSRLPKVLTVVIVFTVOLPY 81

QY 257 NIVKFCRAIDIYLISLTSNCNSKRMIDAIQVTESIALFHSCLNPILYVFMGASKNYMK 316
Db 82 NIVKFCRAIDIYLISLTSNCNSKRMIDAIQVTESIALFHSCLNPILYVFMGASKNYMK 141

QY 317 VAKKYGSWRQRQSVEEFPDSEGPTEPTSTFSI 350
Db 142 VAKKYGSWRQRQSVEEFPDSEGPTEPTSTFSI 175

RESULT 7 US-09-966-755-2
Sequence 2, Application US09966755
Publication No. US200302228A1
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponata, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
FILE REFERENCE: LRS98-16
CURRENT APPLICATION NUMBER: US09/966,755
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 2
LENGTH: 357
TYPE: PRT

QY 197 KALIOMLEICIGFVWFLIMGVCFITARTLMKMPNIKSRLPKVLTVVIVFTVOLPY 256
Db 22 ESDSMLEICIGFVWFLIMGVCFITERTLMKMPNIKSRLPKVLTVVIVFTVOLPY 81

; ORGANISM: Homo sapiens
US-09-966-755-2

Query Match 35.0%; Score 637; DB 9; Length 357;
Best Local Similarity 36.5%; Pred. No. 1e-48;
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

QY 10 DYVYE-NEMGTYDQSQEYLICKIDVREPAKVELVFLTVFVIGLAGNSMVAIAY 68
|| | : | : || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 4 DYGSESTSMDYVNFTDFYCEKNRQFASHFLPPLYLWLVFVGALGNSLVWVY 63

QY 69 YKKORTKDVYTLNLAVALDILLTLPFWAVNAVHGWLKGKIMCKITSALYTLMFVSGMO 128
| : | || : | : || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 CTRVKTMDDMLNLATADLFLEVTLFWAIAADOMKFQPMCKVYNSMFKMFYSCVL 123

QY 129 FLACISIDRYVAVTKVPSQSGVKPCW-----TICFCWVMAATLSPOLVYVTN 179
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 124 LIMCISIVDRYVIAQ----AMRAHTWREKRLLYSKNCFTIWLAALCIPELYSQIK 178

QY 180 DN---ARCPPIFRYLGTSKALIQMELCTIGFVPELIMGVCFITARTLMPNPNTKIS 236
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 179 EESGIAICTMVPSDESTKLKSAVLTKLVILGFLPFLPVVACCYTIITHTLQAKSSKH 238

QY 237 RPLKVLTVVIVTQLPYNVKRCRAIDIYSLTSNCMSKRMIDIAQTWSIALEHS 296
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 239 KALKVITVITVFLSOPNCVNCILLVOTIDAYAFISNCAVSTNIDCFOVTOIAFFHS 298

QY 297 CLNPILYVFMGASFKNYVMKVKYKG 322
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 299 CLNPILYVFMGASFKNYVMKVKYKG 324

RESULT 8
US-09-903-377-2
; Sequence 2, Application US/09903377
; PATENT NO. US20030116727A1

; GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSPENIC MICE CONTAINING CHEMOKINE
FILE REFERENCE: R-365

CURRENT APPLICATION NUMBER: US/09/903, 377

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/217, 255

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/221, 483

PRIOR FILING DATE: 2000-07-27

PRIOR APPLICATION NUMBER: US 60/262, 113

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows version 4.0

SEQ ID NO 2

LENGTH: 357

TYPE: PRT

ORGANISM: Homo sapiens

US-09-952-385-2

Query Match 35.0%; Score 637; DB 10; Length 357;
Best Local Similarity 36.5%; Pred. No. 1e-48;
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

QY 10 DYVYE-NEMGTYDQSQEYLICKIDVREPAKVELVFLTVFVIGLAGNSMVAIAY 68
|| | : | : || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 4 DYGSESTSMDYVNFTDFYCEKNRQFASHFLPFLPVVACCYTIITHTLQAKSSKH 238

QY 69 YKKORTKDVYTLNLAVALDILLTLPFWAVNAVHGWLKGKIMCKITSALYTLMFVSGMO 128
| : | || : | : || : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 CTRVKTMDDMLNLATADLFLEVTLFWAIAADOMKFQPMCKVYNSMFKMFYSCVL 123

QY 129 FLACISIDRYVAVTKVPSQSGVKPCW-----TICFCWVMAATLSPOLVYVTN 179
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 124 LIMCISIVDRYVIAQ----AMRAHTWREKRLLYSKNCFTIWLAALCIPELYSQIK 178

QY 180 DN---ARCPPIFRYLGTSKALIQMELCTIGFVPELIMGVCFITARTLMPNPNTKIS 236
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 179 EESGIAICTMVPSDESTKLKSAVLTKLVILGFLPFLPVVACCYTIITHTLQAKSSKH 238

QY 237 RPLKVLTVVIVTQLPYNVKRCRAIDIYSLTSNCMSKRMIDIAQTWSIALEHS 296
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 239 KALKVITVITVFLSOPNCVNCILLVOTIDAYAFISNCAVSTNIDCFOVTOIAFFHS 298

QY 297 CLNPILYVFMGASFKNYVMKVKYKG 322
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 299 CLNPILYVFMGASFKNYVMKVKYKG 324

RESULT 9
US-09-952-385-2
; Sequence 2, Application US/09952385
; PATENT NO. US20020119504A1

; GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.

APPLICANT: Ponath, Paul D.

TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION

FILE REFERENCE: LKS98-16

CURRENT APPLICATION NUMBER: US/09/952, 385

CURRENT FILING DATE: 2001-09-13

PRIOR APPLICATION NUMBER: 09/266, 464

PRIOR FILING DATE: 1999-03-11

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 357

TYPE: PRT

ORGANISM: Homo sapiens

US-09-952-385-2

Query Match 35.0%; Score 637; DB 10; Length 357;
Best Local Similarity 36.5%; Pred. No. 1e-48;
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

QY 10 DYVYE-NEMGTYDQSQEYLICKIDVREPAKVELVFLTVFVIGLAGNSMVAIAY 68
|| | : | : || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 4 DYGSESTSMDYVNFTDFYCEKNRQFASHFLPFLPVVACCYTIITHTLQAKSSKH 238

QY 69 YKKORTKDVYTLNLAVALDILLTLPFWAVNAVHGWLKGKIMCKITSALYTLMFVSGMO 128
| : | || : | : || : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 CTRVKTMDDMLNLATADLFLEVTLFWAIAADOMKFQPMCKVYNSMFKMFYSCVL 123

QY 129 FLACISIDRYVAVTKVPSQSGVKPCW-----TICFCWVMAATLSPOLVYVTN 179
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 124 LIMCISIVDRYVIAQ----AMRAHTWREKRLLYSKNCFTIWLAALCIPELYSQIK 178

QY 180 DN---ARCPPIFRYLGTSKALIQMELCTIGFVPELIMGVCFITARTLMPNPNTKIS 236
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 179 EESGIAICTMVPSDESTKLKSAVLTKLVILGFLPFLPVVACCYTIITHTLQAKSSKH 238

QY 237 RPLKVLTVVIVTQLPYNVKRCRAIDIYSLTSNCMSKRMIDIAQTWSIALEHS 296
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 239 KALKVITVITVFLSOPNCVNCILLVOTIDAYAFISNCAVSTNIDCFOVTOIAFFHS 298

QY 297 CLNPILYVFMGASFKNYVMKVKYKG 322
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 299 CLNPILYVFMGASFKNYVMKVKYKG 324

RESULT 10
US-10-000-759A-2
; Sequence 2, Application US/10000759A
; PATENT NO. US20030141991A1

; GENERAL INFORMATION:
APPLICANT: Andrew, David P.

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/852,156

FILING DATE: 09-May-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-009NCIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: pigtail macaque

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 31.3%; Score 569; DB 10; Length 342;

Matches 119; Conservative 72; Mismatches 131; Indels 32; Gaps 8;

QY 12 YYEENENGTGTYDYSQEYLICKEDVREFAKVLPFLTIYFVIGLAGNSMVVAIAYKK 71

| : | : | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 6 YHEDYGLNSFDNSQSEE---HQDFLQFRKVFLPCMYLVVFVCGLVNSLVLVISFYHK 61

QY 72 ORTKTDVYIILNAVADLLLFTLPFWAVNAVHWGVWLKGIMCKTSALYTINNSGMQFLA 131

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 62 LQSUTDFLVLNLPLADLIVFCTLPFWAYAGIHEWVFGQVMCKWLGTYTINIFYSMILT 121

QY 132 CTSIDRVYAVKVPSS-OSGVGKPCW--ITCFCVMAAILSLSPOLVFYT--NDNARCI 185

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 122 CITVDRFTIVVVKATKAYNQAKRMTWGKVICLIIWISLVSILPQIITGNVNLDKLIC- 180

QY 186 PIFPRYLGTSMKALIQMLEICIGFWVPLIMGVCFYTPARTLKMNPNIKSRLPKVLTV 245

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 181 ---GYHDKREISTVVLATOMTGLGFPLPLAMTCVSVIKTLHAGGFOKHRSKLTIFLV 236

QY 246 VIVVITVQIPNYIKFCRADIYLISLTSNCMSKRMIDTAQTESIALPHSLNLPIYVF 305

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 237 MAVFLLTQPPFLNKLIRSTHWEVYAMTSFHYT-----IVTEIAVYLRACLNPVLYAF 290

QY 306 MGASFKNYVMVAKKYI-----SRRQRQSYEEFPFDSTGPTPEPTFSI 350

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 291 VSLKFRKNWKLKDIGCIPYLGVSHQWKSSENDSK--TFSASHNVEATSFMQL 342

RESULT 13
US-09-852-156-2

; Sequence 2, Application US/09852156

; Patent No. US20020076941

GENERAL INFORMATION:

APPLICANT: Littman, Dan R.

Deng, Hongkui

Umutmaz, Derya

Ramani, Vineet N.K.

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF

IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

CITY: Hackensack STREET: 411 Hackensack Ave, Continental Plaza, 4th

ZIP: 07601 FLOOR

CITY: Hackensack STATE: New Jersey

COUNTRY: USA

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/852,156

FILING DATE: 09-May-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-009NCIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-852-156-2

Query Match 30.8%; Score 560; DB 10; Length 342;

Matches 117; Conservative 33.1%; Pred. No. 5.9e-42; Indels 32; Gaps 8;

QY 12 YYEENENGTGTYDYSQEYLICKEDVREFAKVLPFLTIYFVIGLAGNSMVVAIAYKK 71

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 6 YHEDYGRSSFDNSQSEE---HQDFLQFSKVLPCMYLVVFVCGLVNSLVLVISFYHK 61

QY 132 CTSIDRVYAVKVPSS-OSGVGKPCW--ITCFCVMAAILSLSPOLVFYT--NDNARCI 185

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 62 CITVDRFTIVVVKATKAYNQAKRMTWGKVICLIIWISLVSILPQIITGNVNLDKLIC- 180

QY 72 ORTKTDVYIILNAVADLLLFTLPFWAVNAVHWGVWLKGIMCKTSALYTINNSGMQFLA 131

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 61 LQSUTDFLVLNLPLADLIVFCTLPFWAYAGIHEWVFGQVMCKWLGTYTINIFYSMILT 121

QY 186 PIFPRYLGTSMKALIQMLEICIGFWVPLIMGVCFYTPARTLKMNPNIKSRLPKVLTV 245

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 181 ---GYHDKREISTVVLATOMTGLGFPLPLAMTCVSVIKTLHAGGFOKHRSKLTIFLV 236

QY 246 VIVVITVQIPNYIKFCRADIYLISLTSNCMSKRMIDTAQTESIALPHSLNLPIYVF 305

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 237 MAVFLLTQPPFLNKLIRSTHWEVYAMTSFHYT-----IVTEIAVYLRACLNPVLYAF 290

QY 306 MGASFKNYVMVAKKYI-----SRRQRQSYEEFPFDSTGPTPEPTFSI 350

| : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | |

Db 291 VSLKFRKNWKLKDIGCIPYLGVSHQWKSSENDSK--TFSASHNVEATSFMQL 342

RESULT 14
US-09-940-063-2

; Sequence 2, Application US/09940063

; Patent No. US20020090657A1

GENERAL INFORMATION:
 APPLICANT: Briskin, Michael J.
 APPLICANT: Murphy, Kristine E.
 APPLICANT: Wilbanks, Alyson M.
 APPLICANT: Wu, Lijun
 TITLE OF INVENTION: No. US2002009057A1el Antibodies and Ligands for "Bonzo"
 FILE REFERENCE: 1855.1070-000
 CURRENT APPLICATION NUMBER: US/09/940,063
 PRIORITY APPLICATION NUMBER: 09/449,437
 PRIOR FILING DATE: 1999-11-24
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 342
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-940-063-2

Query Match 30.8%; Score 560; DB 10; Length 342;
 Best Local Similarity 33.1%; Pred. No. 5_9e-42; Mismatches 117; Indels 32; Gaps 8;
 Matches 17; Conservative 75; MisMatches 130; Indels 32; Gaps 8;
 QY 12 YYEERENEMGTYDYSQVELCIIKEDREPAKEVFLPFLTIVETGLAGNSMVAIAYKK 71
 DB 6 YHEQYGFSSFNDSQQEE--HODFLQFSKVKFLPCMLVNFVGLVNSLVLVISIFYHK 61
 QY 72 QRTKDQVYILNLAVALDLLETFPPFWANAVHGWLKGIMCKITSALYTLPNGMFLA 131
 DB 62 LQSLJTDVFLVNLPLADLVFLVCTLPFWAYAGIHWNVFGQVMCKSLLGITYTINFTSMLLT 121
 QY 132 CISDRYVAVTKPS--QSGVGPRCW--IICFCWMAILLSIPOLVFTV-NDNRCI 185
 DB 122 CIVDRETFIVVKAHKAYNOAKRMTWGVTSLLWISLVSIPOLIYGNVFLDKLC- 180
 QY 186 PIFPRYPLGSMKAIQMLEICIPFVFLPFLIMGVCFITARTLMKMPNIKISRPKVLIY 245
 DB 181 ---GYHOBIAISITVVLATQMTLGFPLFLPFLTMIVCYSVIKLTHAGGFQKHSLSKTLFLY 236
 QY 246 VIVFTIVTOLPYNTVFKCRAIDIYLSLTSNCNNKRMIDIAQVESTALFHSCNPLILVF 305
 DB 237 MAVFLIOPFMKMFIRSTHWIYAMISHTI-----INVTEATAYLRACLNPNLYAF 290
 QY 306 MGASFKNYVNMVKVKG-----SRRQRQSVEFPDSEGPPTPSI 350
 DB 291 VSLKFRKFNWKLYKDGLCPYLGVSHQWSSEDDNSK--TESASHNVEATSMPQL 342
 RESULT 15
 US-10-120-394-20

SEQUENCE CHARACTERISTICS:
 LENGTH: 360 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 US-10-120-394-20

Query Match 29.5%; Score 537.5; DB 9; Length 360;
 Best Local Similarity 35.8%; Pred. No. 6e-40; Mismatches 115; Indels 19; Gaps 6;
 Matches 115; Conservative 63; MisMatches 124; Indels 19; Gaps 6;
 QY 10 DYVYERENEMGTYDYSQVELCIIKEDREPAKEVFLPFLTIVETGLAGNSMVAIAYKK 69
 DB 8 DTLDKSIYNNVLYESIPPCTKEKGIAKGELFLPPLYSLVFGFLGNSVWVLVLFKY 67
 QY 70 KQORTKTDQVYILNLAVALDLLETFPPFWANAVHGWLKGIMCKITSALYTLPNGMFL 129
 DB 68 KRLRSMDTVDVLLNLAISDLFLVFLSPFWGQYAADQWVFGLGCKNMISWNYLVGFYSGIFF 127
 QY 130 LACISDRYVAVTKV----PSOSGVGPRCWITFCFCWMAILLSIPOLVFT-YVN 179
 DB 128 VNLMSIDRYLAIVHAVFSLRARTLRYGV----ITSLARWWSVAVFASELPGFLSTCYTER 182
 QY 180 DNARCPIPFPRYPLGSMKAIQMLEICIPFVFLPFLIMGVCFITARTLMKMPNIKISRP 238
 DB 183 NHTYCKTKS--LNSITWKLSSLBENILGFLVPLGIMCYSBIRLQHCKNEKKKA 240
 QY 239 LKVLTIVVIVTIVTOLPYNTVFKCRAIDIYLSLTSNCNNKRMIDIAQVESTALFHSCL 298
 DB 241 VRMIFAVWVFLGFWTIPYVFLTL-VLELVQDCITFERYDIAQATETLAFVHCCL 299
 QY 299 NPILYVFMGASFKNYVNMVKVAK 319
 DB 300 NPIIYFLGEKERKYVILQFLK 320

Search completed: March 14, 2003, 16:16:55
 Job time : 16 secs

GENERAL INFORMATION:
 APPLICANT: Wells, Timothy N.C.
 APPLICANT: Power, Christine A.
 TITLE OF INVENTION: CHEMOKINE RECEPTOR ABLE TO BIND TO MCP-1, MCP-1 ALPHA AND/OR RANTES AND ITS USES
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHIE P.C.
 STREET: 1100 No. US20020160015A1th Glebe Rd. 8th floor
 CITY: Arlington
 STATE: VA
 COUNTRY: USA
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/120,394

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model
Run on: March 14, 2003, 16:11:03 ; Search time 32 Seconds
(without alignments)

2253.640 Million cell updates/sec

Title: US-09-686-020A-2
Perfect score: 1819
Sequence: 1 MALEONQSTDDYYEENEMNG VEEFFFDSEGTEPTISTFSTI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21i:
1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

Result No. Score Query Length DB ID Description

Result No.	Score	Query	Length	DB	ID	Description
1	1596	87.7	350	11	Q924T3	Q92413 mus musculus
2	1593	87.6	350	11	Q8QZB3	Q8QZB3 mus musculus
3	912	50.1	221	11	Q8ESK1	Q8ESK1 rattus norvegicus
4	643	35.3	369	4	Q9UQ66	Q9UQ66 homo sapiens
5	611	33.6	367	11	Q9R1V0	Q9R1V0 mus musculus
6	586.5	32.2	368	13	Q42444	Q42444 oncorthynchus
7	578	31.8	343	6	Q9N0Z0	Q9N0Z0 cercopithecus
8	566.5	31.1	351	11	Q9EQ06	Q9EQ06 mus musculus
9	566	31.1	343	6	Q9BD56	Q9BD56 macaca fasciata
10	561.5	30.9	351	11	Q9ERH5	Q9ERH5 mus musculus
11	560	30.8	342	4	Q9HC55	Q9HC55 homo sapiens
12	559	30.7	342	6	Q9TV16	Q9TV16 pan troglodytes
13	544	29.9	358	13	Q9PA00	Q9PA00 acipenser ruber
14	534.5	29.4	360	11	Q9IZH4	Q9IZH4 rattus norvegicus
15	529	29.1	361	11	Q8VRH3	Q8VRH3 cavia porcellus
16	520.5	28.6	358	13	Q9YGC3	Q9YGC3 xenopus laevis

Database : SPTREMBL_21i:
1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Database : SPTREMBL_21i:
1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

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12: sp_virus:*

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17: sp_archaea:*

Database : SPTREMBL_21i:
1: sp_archea:*

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3: sp_fungi:*

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6: sp_mammal:*

7: sp_mhc:*

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12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Database : SPTREMBL_21i:
1: sp_archea:*

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3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Database : SPTREMBL_21i:
1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

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11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Database : SPTREMBL_21i:
1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

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9: sp_phage:*

10: sp_plant:*

11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Database : SPTREMBL_21i:
1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Database : SPTREMBL_21i:
1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Database : SPTREMBL_21i:
1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Database : SPTREMBL_21i:
1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

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12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Database : SPTREMBL_21i:
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4: sp_human:*

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6: sp_mammal:*

7: sp_mhc:*

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10: sp_plant:*

11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

Database : SPTREMBL_21i:
1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_reptile:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*</p

Db :||||||||||||||||||||||||||||||||||||||||| 120
 61 VVAVIAYAKKQRKTVDILNLAVADLILITLPFWAVNAVHGWLGRMKCKVTSALYT 120
 QY 121 LNFTVSGMQLACISIDRYVAVTKVPSQSGVGKPCWICFCVNMAAILSPOLVFVYND 180
 :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :|||||||
 Db 121 VNFTVSGMQLACISIDRYVAVTKVPSQSGVGKPCWICFCVNMAAILSPOLVFVYND 180
 QY 181 NRCIPIPRFLGTSKALIQMLEICIGFWPPFLMGCVYFIRTLMKMPNPKISRPLK 240
 :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :|||||||
 Db 181 NRCPTPIPHLGSLSKASIOLEIGIGFWPPFLMGCVYASTARALTKMPNPKSRPLR 240
 QY 241 VLTVVIVFLVTPQIYNTVKCRAIDITYSLTSCNMKRMDDAIQTESIALFHSLNP 300
 :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :|||||||
 Db 241 VLAVVWVFVTPQIYNTVKCRAIDITYSLTSCNMKRMDDAIQTESIALFHSLNP 300
 QY 301 ILYVFMGASFKNYIMKVAKYKGSRQRQSVFPESEGPFEPSTSFI 350
 :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :|||||||
 Db 301 ILYVFMGASFKNYIMKVAKYKGSRQRQSVFPESEGPFEPSTSFI 350
 OC ||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :|||||||
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Rattus norvegicus (Rat).
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HARLAN_SPRAGUE-DANLEY;
 RA Carroll S.L.; Miller M.L.; Benedict-Hamilton H.M.;
 RT "Identification and characterization of novel G-protein coupled
 receptors expressed in regenerating peripheral nerve.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 DR PRINTS: PRO0237; GPCR_Rhoopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECCEP_F1_2; 1.
 DR Receptor.
 FT NON_TER 1 1
 FT NON_TER 221 AA; 221
 SQ SEQUENCE 221 AA; 2434 MW; 5622DP607373846C CRC64;
 Query Match 50.3%; Score 912; DB 11; Length 221;
 Best Local Similarity 83.3%; Pred. No. 4e-75; ID: 1.
 Matches 169; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
 RT Townson J.R., Nibbs R.J.:
 RT "Characterization of mouse CX CR, a receptor for the lymphocyte-
 attracting chemokines TECK (CCL25), SLC (CCL21) and MIP-3beta (CCL19):
 RT comparison to human CX CRK";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY072976; AL068400; 1;
 DR EMBL; AY072938; AL068462; 1;
 KW Receptor.
 SQ SEQUENCE 350 AA; 3954 MN; D017CC29749CECD5 CRC64;
 Query Match 87.6%; Score 1593; DB 11; Length 350;
 Best Local Similarity 85.1%; Pred. No. 7.5e-13; ID: 1.
 Matches 298; Conservative 27; Mismatches 25; Indels 0; Gaps 0;
 RT 1 MALEONQSTDYYEENEMGTYPSQELICTKEDVREFAKYELPVLTIVFVLAGNS 60
 QY 1 MALELNQSAEYYEEENEMYTHDSOYEVICIREKEVROFAKVELPAFFTVAFTVLAGNS 60
 QY 61 MVVAVIAYAKKQRKTVDYLNLAVADLILFLPFWAVNAVHGWLGRMKCKVTSALYT 120
 :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :|||||||
 Db 61 VVAVIAYAKKQRKTVDYLNLAVADLILFLPFWAVNAVHGWLGRMKCKVTSALYT 120
 QY 121 LNFTVSGMQLACISIDRYVAVTKVPSQSGVGKPCWICFCVNMAAILSPOLVFVYND 180
 :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :|||||||
 Db 121 VNFTVSGMQLACISIDRYVAVTKVPSQSGVGKPCWICFCVNMAAILSPOLVFVYND 180
 QY 181 NRCIPIPRFLGTSKALIQMLEICIGFWPPFLMGCVYFIRTLMKMPNPKISRPLK 240
 :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :|||||||
 Db 181 NRCPTPIPHLGSLSKASIOLEIGIGFWPPFLMGCVYASTARALTKMPNPKSRPLR 240
 QY 241 VLTVVIVFLVTPQIYNTVKCRAIDITYSLTSCNMKRMDDAIQTESIALFHSLNP 300
 :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :|||||||
 Db 241 VLAVVWVFVTPQIYNTVKCRAIDITYSLTSCNMKRMDDAIQTESIALFHSLNP 300
 OC ||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :||||||| :|||||||
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99248139; PubMed=10229797;
 RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RT Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
 receptor for the chemokine TECK.;

QY 71 KQ-RKTDVYILNLAVALDLILFLPFWAVIAVHGWGLKGIMCKITSALYTINFLVSGMQF 129
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 77 ORQKTMDFYLNLNLAVALDLEFLGTLPLWAVANQWSMGLGCKTISAFKINFESSMLI 136
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 130 LACISIDRYAVTKVPSQSGVGKP---CWLTFCVMAITLSPOLVFTVND---NA 182
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 137 LTCISIDRYVYIVTMAQNSKRQLCSKCVCACWLAVLALPEFMFRANKELDQF 196
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 183 RCIPFPRLGTSMMALIQMEICIGFVVFPLIMGVCFITARTLMKMPNKTISPLK 242
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 197 YCTMVIWSNQNRTKIVLGLQICMGCPCLPLVMVFCYAGIRTIRLKLTRSPKHKALRV 256
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 243 LTWVIVFIVTOLPYNPKERADIYSLTSNCNNSKRMQTAIQTESTIALFHSCINPL 302
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 257 LVVAVFVFLSQLPVNVLVHATQAANSTQDCSAAKRFNVSOYLVSLAYTHACLNP 316
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 303 YVFMGAASKVYKVKAKKVYSW 324
 :: :|||:|||:|||:|||:
 Db 317 YVFVGVFRRLKLLRHYHW 338
 :: :|||:

RESULT 7

O9N0Z0 PRELIMINARY; PRT; 343 AA.
 AC Q9N0Z0;
 DT 01-OCT-2000 (TREMBrel. 15, created)
 DT 01-OCT-2000 (TREMBrel. 15, last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE STR33.
 OS cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC Cercopithecinae; Cercopithecidae;
 OC NCBITAXID=9531;
 RN [1]
 SEQUENCE FROM N.A.
 MEDLINE-20261727; PubMed=1079581;
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RA "Simian immunodeficiency virus utilizes human and sooty mangabey but
 RT not rhesus macaque STR33 for efficient entry.",
 RL J. Virol. 74:5075-5082(2000).
 DR InterPro; IPR000216; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCR_RHODOPSN.
 DR PRINTS; PRO1568; LIMPHOTACTNR.
 DR PROSITE; PS05062; G_PROTEIN_RECEP_FL1; UNKNOWN_1.
 DR PROSITE; PS0237; G_PROTEIN_RECEP_FL2; 1.
 DR Receptor.
 RN SEQUENCE FROM N.A.
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 EMBL; AF237559; AAF68392.1; -.
 InterPro; IPR00276; GPCR_Rhodpsn.
 Pfam; PF00001; 7tm_1; 1.
 PRINTS; PRO0237; GPCR_RHODOPSN.
 DR PROSITE; PRO1568; LYMPHOTACTNR.
 DR PROSITE; PS0237; G_PROTEIN_RECEP_FL1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_FL2; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_FL1; UNKNOWN_1.
 SEQUENCE 343 AA; 3959 MW; A75BA0751C13455 CRC64;

Query Match 31.8%; Score 566.5; DB 11; Length 351;
 Best Local Similarity 35.4%; Pred. No. 1.7-43;
 Matches 127; Conservative 70; Mismatches 125; Indels 37; Gaps 1;
 QY 10 DYVYEEEN-EMNGTYDQYQVELCIKEDVR-EFAVKFLPVLFITVIGLAGNSMVAY 65
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 12 DGYEGDFWLFVNNSDANSQ-----ENKFLKEVFLPCVYLWVFVGLGNLSVLI 64
 QY 66 YAVKKQRKTDVYILNLAVALDLILFLPFWAVNAVHGWGLKGIMCKITSALYTINFLVFS 125
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 65 YIFYOKRLHTDVFLNLNPFLADLFLVFCYPLFWAGYTFEWFGCTLRGMYTMYFV 124
 QY 126 GMQFLACLSIDRYAV --TKVPSQSGVGKPW---ICFCVMAITLSPOLVFTVND 180
 :: :|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 125 SMLTCLTCITVDRETFIVVQATAFNROKWK-IWGOVTCILWVSLVLSPLQIYHQD 183
 QY 181 NARCIPFPRLGTSMMALIQMEICIGFVVFPLIMGVCFITARTLMKMPNKTISPLK 240
 :: :|||:|||:|||:|||:|||:|||:|||:|||:
 Db 184 TDKLI---CQHSEESTIMVLYQMTIGFFPLLTMVLCYSGIKLHLHARNFKHSLK 240
 QY 241 VLTWVIVFIVTOLPYNPKERADIYSLTSNCNNSKRMQTAIQTESTIALFHSCINPL 300
 :: :|||:|||:|||:|||:|||:|||:|||:|||:
 Db 241 IIFLVVAVFLRQTPFLNPLMLQSTSWEYTT-----FKAIVWTEAYFRACLN 294
 QY 301 YVFMGAASKVYKVKAKKVYSW-----SWRRQRQSVEFPFDSEGPPETSTS 350
 Db 295 VLYAFVGLKFRKNWKLMDKGCLSHLGVSQSSWKSSEDSK--TGSASHNVEETSMQL 351

DR EMBL; AF029759; AAG21918; 1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF0001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCR_RHODOPSN.
 DR PROSITE; PRO1568; LYMPHOTACTNR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor. 342 AA.; 39279 MW; CE149633D01D20AA CRC64;
 SQ SEQUENCE

Query Match	30.8%	Score 560; DB 4;
Best Local Similarity	33.1%	Length 342;
Matches	117;	Conservative 75; Mismatches 130; Indels 32; Gaps 8;
Db	6 YHEDYGFNSFNDSSQEE--HQDLOFSKVFLPCMVLVVFGLVGNSLVLSIFYHK	

Qy 12 YYEENEMGNTDYDSQYELICIKEDREFAKVFLPFLTVFVIGLAGNSMVAY 71
 Db 6 YHEDYGFSSFNDSQEE--HQDLOFSKVFLPCMVLVVFGLVGNSLVLSIFYHK 61

Qy 72 QRMKTDVYLNLAVADLLFLPFRANVHWGVWKGKMKTSALYTINFVSGMQFLA 131
 Db 62 LOSLTDFLVNLPLADLFLVCFLPLPMQVAGIHEWVFGQVMCKSLIGIYTNPYEMILIT 121

Qy 132 CISIDRYVAVTKVPS - QSGVSKPCW - IICPCVMAAILSLSPOLVYTV - NDNARCI 185
 Db 122 CITVDRFIVVVKATKAVNQAKRMTGWKVTLWVSLVSPQIYGNGVFLNLDKLIC - 180

Qy 186 PIFPRYLGTSMKALIQMLEICIGFVVPPFLMGCVCFITARTLMMKPNTRISRDPLKLVLY 245
 Db 181 ---GYHDEAISTVVLATQMLTGFPLPLTMVCSVIKTLHAGGFOKRHSKLIIFLY 236

Qy 246 VIVFTIVOLPYNIVKFCRAIDIYSLTSNCNSMRNDIAQTESIALFHSCNPLVLF 305
 Db 237 MAVFLLTOMPLNLMKFIRSTHWEYIAMSFSHYI-----IMVIAIAVLRACLNPVLYAF 290

Qy 306 MGASFKNVWKVAKYKG-----SWRRQRQSYVEFPFDSDGGPTETSTFSI 350
 Db 291 VSLKFRKNFWKLVKDIGCLPYLGVSHOWKSSEDNSK--TFSASHNVEATSMFQL 342

RESULT 12

Q9TV16 PRELIMINARY; PRT; 342 AA.

ID Q9TV16 AC Q9TV16; PRELIMINARY; PRT; 342 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE G protein-coupled receptor STRL33.

OS Pan troglodytes (Chimpanzee).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae; Acipenser.

OC NCBI_TaxId=7906;

RN [1] RESULT 13

RP SEQUENCE FROM N.A.

ID Q9RUAO AC Q9RUAO; PRELIMINARY; PRT; 358 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE CXCR chemokine receptor 4.

CC CXCR4.

OS Acipenser ruthenus (sterlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae; Acipenser.

OC NCBI_TaxId=7906;

RN [1]

RP SEQUENCE FROM N.A.

ID MEDLINE=20368347; PubMed=10906389;

RA Alabyev B.Y., Najakshin A.M., Mechetina L.V., Taranin A.V.;

RT "Cloning of a CXCR4 homolog in chondrostean fish and characterization of the CXCR4-specific structural features.", Dev. Comp. Immunol. 24:765-770(2000).

RL -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR EMBL; AJ249438; CAB60252; 1; -

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF0001; 7tm_1; 1.

DR PRINTS; PRO1558; CHEMOKINER11.

DR PRINTS; PRO0237; GPCR_RHODOPSN.

DR PROSITE; PRO1568; LYMPHOTACTNR.

DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.

DR PROSITE; PS50262; G_protein_coupled_receptor_Glycoprotein; Receptor; transmembrane.

SQ SEQUENCE 358 AA; 4048 MW; 7B3B99B962453008 CRC64;

Query Match 29.9% Score 544; DB 13; Length 358;
 Best Local Similarity 35.5%; pred. No. 1.9e+11; Indels 18; Gaps 7;

Matches 125; Conservative 64; Mismatches 145; Indels 18; Gaps 7;

Db 67 ATYYKORKTQYVNLAVADLLFLPFRANVHWGVWKGKMKTSALYTINFVSG 126

Db 67 G-YQKRTMTDKYRLHLIADDLFLVFTLPFWADRASSWVFFGLICKIVNISIYTVNLS 125

Qy 127 MOFLACISIDRYVAVTKVPSQSGVGRCP---WTCFCVMAAILSLSPOLVYTVND 181
 Db 126 VLTAFISFDRYLAVV RATNSH--KPRKLLAEKIIVGVWLPATLLTVPDLVFAQVHDE 182

Qy 30.7% Score 559; DB 6; Length 342;
 Best Local Similarity 33.1%; pred. No. 7.8e+43;
 Matches 117; Conservative 74; Mismatches 131; Indels 32; Gaps 8;

Db 126 YYEENEMGNTDYDSQYELICIKEDREFAKVFLPFLTVFVIGLAGNSMVAY 71

QY 182 A---RCIPIFPRVIGTSMKALIQMLECIGFVVFPLIMGVCVFFITARLMK-MPNIKSR 237
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 183 GTRAMCDRVPSPESGNNTMIFRRQHITFVGVLVPGLVITCKCIIITKLSDGSKGFLKRR 242
 QY 238 PLKVLTIVVIVFVTOPLNPVNIVFCRAIDIYSLITSNMSKRMIDIAQYTESI 297
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 243 ALKTTTILLAFICWLPCYATLVDTLVILNVNQYNTLQHHMETWIFVTEGLAYFHCC 302
 QY 298 LNPILYVENGASFKNYVMVKVKGSMRQRSSVEEPPDSGPTERTSFS 349
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 303 LNSTLYARTGVK---KSAKALTNSRGSSKILSKNKKGGLSVSTES 350
 QY 304 LNPILYVENGASFKNYVMVKVKGSMRQRSSVEEPPDSGPTERTSFS 350
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 305 LNSTLYARTGVK---KSAKALTNSRGSSKILSKNKKGGLSVSTES 350
 RN RESULT 14
 Q91H4 PRELIMINARY; PRT; 360 AA.
 ID Q91H4 PRELIMINARY; PRT; 360 AA.
 AC 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 20, Last sequence update)
 DE C-C chemokine receptor 4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN="EW";
 RA Garcia G.E., Chen S., Xia Y., Harrison J., Wilson C.B., Johnson R.J.,
 RA Bacon K.B., Feng L.;
 RT "Mononuclear cell-infiltrate inhibition by blocking macrophage-derived
 chemokine results in attenuation of developing crescentic
 glomerulonephritis.",
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF32872; AL30398.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO1559; DuffyAntigen.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_FL1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_FL2; 1.
 KW Receptor.
 SEQUENCE 360 AA; 41218 MW; 5095C6CD299E1F8B CRC64;
 Query Match 29.4%; Score 534.5; DB 11; Length 360;
 Best Local Similarity 34.7%; Pred. No. 1.4e-40;
 Matches 113; Conservative 67; Mismatches 127; Indels 19; Gaps 6;
 QY 3 LEQNSTDYYENEMNGTYDYSQYELCICKEPVRFKAVLPLVFTIVEVIGLAGNSMVAIY 62
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 1 MNATEVTDITQDETEYNSYFDSLPLPKCTKEGIKAFGEVLEPLPLYSLVFLGLFGMSVV 60
 QY 63 VATAYVKKORTKDWTYIINLAVADLLFTEFWAVNAVHWKWLGMCKTSALYTIN 122
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 64 VLVLPKYRKLSKMPDVYLNLALISDLFVLSLFWGYYAODWVFGLGCKITSWMVLYG 120
 QY 123 FVSGMQLFLACISIDRYAVAKV-----PSQSGVGPCKWCIIIFCFVMAAILSLIPOLVF 175
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 124 FVSGIFFTIMMSIDRYLAIVHAFSLRARTLVGV-----ITSLIWSVAFASTPGLF 175
 QY 176 YTV---NDMARCTIPFPRVIGTSMKALIQMLECIGFVVFPLIMGVCVFFITARLMKMP 231
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 176 STCDTENNHTTYCKTQS -VNSTWKVLISSLNEIIVGLVPLGIMLFCYSMIRTLRHCK 233
 QY 232 NIKISRPLVLTIVVIVFVTOPLNPVNIVFCRAIDIYSLITSNMSKRMIDIAQYTESI 291
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 234 NEKKNRARVAVVAVVLFGLFWTFPYNVVLFLETL-VELEVLOQDCTLERYDIALQATEL 292
 QY 292 ALFHSCINPILYVEMGASEKYYVMVK 319
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 293 AFIHCCLNPIVYFFLGEGFRKYIVQL 318

RESULT 15
 Q8VHP3 PRELIMINARY; PRT; 361 AA.
 ID Q8VHP3; PRELIMINARY; PRT; 361 AA.
 AC 08VHP3; PRELIMINARY; PRT; 361 AA.
 RT "The identification, characterization and distribution of guinea pig
 CCR4 and epitope mapping of a blocking antibody.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF431971; AAL57489.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO0237; GPROTEINRECEPFL1; UNKNOWN_1.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_FL2; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_FL2; 1.
 SQ SEQUENCE FROM N.A.
 RA Jopling L.A., Sabroe I., Andrew D.P., Mitchell T.J., Li Y.,
 RA Hodge M.R., Williams T.J., Pease J.E.,
 RT "The identification, characterization and distribution of guinea pig
 CCR4 and epitope mapping of a blocking antibody.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF431971; AAL57489.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO0237; GPROTEINRECEPFL1; UNKNOWN_1.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_FL2; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_FL2; 1.
 SQ SEQUENCE 361 AA; 41064 MW; 9304E897D4FD6839 CRC64;
 Query Match 29.1%; Score 529; DB 11; Length 361;
 Best Local Similarity 36.0%; Pred. No. 4.4e-40;
 Matches 118; Conservative 66; Mismatches 104; Indels 40; Gaps 10;
 QY 9 TDYYEENEMNTYDYSQYELCICKEPVRFKAVLPLVFTIVEVIGLAGNSMVAIY 68
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 17 SNYYNEESSVPGP-----CTKIGVAFGELEPLPLPLSVELFGLGNSVVVVLFLK 67
 QY 69 YKKRRTDVTWLNIAVADDLILFPTPFWAVNAVHWGWLKGKMCITSAYTAATLNEVSQGQ 128
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 68 YKRLRSMTDWVLLNIAISDLIELFVLSLPFWSYAAQWNFGWLGKCMISWVLYFSGF 127
 QY 129 FLACTISDRYYAVT-----KVPSSOS-GVKRPCWCITCFCWMAATLTSIQLVF--YV 178
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 128 FTVLMSIDRYLAIVHGVSFSMRVRFITYGV----ITSLATWAWVAFASLGLLFLSTCYIE 182
 QY 179 NDNARCPFPRVLYGNSMK-AIQLMEI-CIGFVVFPLIMGVCVFFITARLMKMPNIKS 236
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 183 RNHTSC---KTRYSANSTTWKVLSSLEINTLGLVPLGIMLFCYSMIRTLQHCKSKKRN 239
 QY 237 RDLKVLVTVVIVFVTOPLNPVNIVFCRAIDIYSLITSNMSKRMIDIAQYTESI 291
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 240 KAVKMFIAVWVFLGLFWTFPWVNLV-----LYTLEVELEVLQDCSLEYDIALQATEL 293
 QY 292 ALFHSCINPILYVEMGASEKYYVMVK 319
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 294 AFIHCCLNPIVYFFLGEGFRKYIVQL 321

Search completed: March 14, 2003, 16:13:21
 Job time : 37 secs

